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acquences have been round to be highly momologous to a human lympholog cell activation antigen designed CD39 (Maliszenski et at. (1994). J. Immunol.: 3574-3583). The complete sequences of the AFPDases types I and II have not been obtained yet. Assuming that the CD39 gene product is an AFDBase type II, the use of CD39 in the reduction of platelet aggregation and of thrombogenicity may be contemplated, as well as a process of making AFPDases using the CD39 sequence (AAT38516)
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Compugen Ltd.
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Human soluble CD39 protein
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 N-PSDB; AAT33966
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ATP diphosphohydrolase; transgenic animal; pig; porcine;
transplantation; endothelial cell; prosthetic device;
platelet aggregation; inhibition; intravascular.
 Length
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Query Match 100.0%; Score 2698; DB 2; Best Local Similarity 100.0%; Pred. No. 5.2e-262; Matches 510; Conservative 0; Mismatches 0;
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therapy of inflammatory or immunological stimulation of platelet sgation - using CD39 protein with ATP di:phospho:hydrolase activity, al for preventing or alleviating thrombotic condition in mammalian
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100.0%; Pred. No. 5.2e-262;
ive 0; Mismatches 0;
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                                                                                                                                                         Claim 3; Page 39; 65pp; English
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Sequence 510 AA;

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Solubbe CD39; human; apyrase activity; platelet activation; inhibitor; unstable angina; myocardial infarction; stroke; oconary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coggulopathy; deep venous thrombosis; DY; pulmonary embolism; PE; thrombus formation; occlusion; stenosis; restenosis; angiogenesis; antianginal; cerebroporotective; antiarteriosclerotic; anticoagulant;
                                                                                                                                                                                                                                                 457. .459
/note= "Asn is N-glycosylated"
477. .499
/label= Transmembrane 2---
                                                                                                                                                                                     note= "Asn is N-glycosylated"
92. .294
                                                                                                                                                                   "Asn is N-glycosylated"
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/note= "C-terminal end"
                                                                                                                        17. .37
/label= Transmembrane_dk
/note= "N-terminal end"
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                                                                                                                 Location/Qualifiers
                                                                            cardiant; vasotropic; thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim la; Fig 1; 122pp; English.
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98US-0107466P.
99US-0149010P.
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/note= "Asi
371. .373
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                                                                                                                                                                            .229
                                                                                                                                                                    note=
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                                                                                                                             Domain
                                                                                                                                                                                                                                                                             Domain
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The present sequence is the human soluble CD39 protein, a cell surface molecule, having apyrase activity. It is derived from a human B cell line constructed by referred to as MP-1. Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and cerevity including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting angiogenesis. It is useful for the treatment of unstable angina, myocardial infartcion, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preclampsia, embolism, platelet-associated ischaemic disorders including lung, coronary and cerebral ischaemia, thrombotic disorders including coronary, peripheral and creabral artery thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PB) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, seconlasion, seconlasion, seconlasion, seconlasion, seconlasion, seconlasion, seconlasion, seconlasion, and secondary and serventing thrombus formation or reformation, occlusion, reocclusion, New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury.

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SLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNBIGIYLTDCMERAREVIPRSQ 120
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                                                                                         1 MEDIKESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHT
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                                     Gaps
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   Length 510;
                                   Indels
Score 2698; DB 3;
Pred. No. 5.2e-262;
; Mismatches 0;
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/labbl= Transmembrane_domain
73. .75
/note= "Asn is N-glycosylated"
227. .229
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 100.0%;
100.0%;
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Query Match
Best Local Similarity 100.
Matches 510; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39
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          292. .294
/note= "Asn is N-glycosylated"
334. .336
                                         /note= "Asn is N-glycosylated" 371. .373 /note= "Asn is N-glycosylated" 457. .459
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/note= "Asn is N-glycosylated"
"Asn is N-glycosylated"
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/label= Transmembrane_domain
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98US-0107466P.
99US-0149010P.
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RES FOUND INC
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nes 510; Conservative
  note₌
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                                                                                                                                                                                                                                                                    (IMMV ) IMMUNEX
(CORR ) CORNELL
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                                                                                                                                              WO200023094-A2
           Modified-site
                                  Modified-site
                                                          Modified-site
                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides.
                                                                                                                                                                                             13-OCT-1999;
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06-NOV-1998;
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The present sequence is the human CD39 polypeptide. The present sequence or its active fragment may be administered to treat or prevent stroke in a subject susceptible to intracranial haemorrhaging or an ischaemic disorder. The CD39 polypeptide inhibits ADP-mediated platelet aggregation or leukcoyte accumulation and/or ATP by increasing ADP catabolism to the subject. It is useful for treating or preventing stroke, thrombotic disorders and ischaemic disorders such as peripheral vascular disorder, pulmonary embolus, venous thrombosis, myocardial infarction, transient ischaemic attack, unstable angina, reversible ischaemic neurological deficit and sickle cell anaemia. It is also useful for treating or preventing a stroke disorder in a subject undergoing heart surgery, lung surgery, spinal surgery, brain surgery, vascular surgery, abdominal surgery, or organ transplantation surgery
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181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFR 240
                                                                            LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; CD39; vasotropic; cerebroprotective; haemostatic; thrombolytic; stroke; thrombotic disorder; ischaemic disorder.
                                                                                                                                                                                                                              CTKRFEMTLPFQOFE1QG1GNYQQCHQS1LELFNTSYCPYSQCAFNG1FLPPLQGDFGAF
                                                                                                                                                                                                                                                                         CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAF
                                                                                                               LYGKDYNVYTHSFLCYGKDQALMQKLAKDIQVASNEIILRDPCFHPGYKKVVNVSDLYKTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB71917 standard; protein; 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYCO ) UNIV COLUMBIA NEW YORK.
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SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
                  19-FEB-2003; 2003WO-US004845
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 510 AA;
28-AUG-2003
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                                                                                            SLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQ
                                                                                                                                 HQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWI
                                                                                                                                                                       TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFR
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                                            MEDTKESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHT
                                                             MEDTKESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHT
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        Length
                           Indels
       Score 2698; DB 4;
Pred. No. 5.2e-262;
Mismatches 0;
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/note = ACR1

125. .135

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171 . .183

/note = ACR3

213 . .220
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447. .454
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/note = ACR5
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                1 Similarity 100.
510; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003070823-A2
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Matches 510
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The invention relates to a conjugate (I) comprising an enzyme and a biodegradable polymer, where (i) enzymatic activity of the enzyme is higher relative to that of the enzyme in the absence of the biodegradable polymer, or (ii) the half life of the enzyme is longer than that of the enzyme in the absence of the polymer. The enzymatic activity (i) is at enzyme in the absence of the polymer. The enzymatic activity (i) is at polymer. The enzyme higher in the presence of the polymer. The enzyme is a multimeric, soluble and/or extracellular enzyme, preferably an apyrase, especially a soluble form of CD39 and catalyzes hydrolysis of nucleoside diphosphate. The conjugate can be used to treat diseases relating to abnormal levels of extracellular nucleotides or abnormal aggregation of platelets, particularly cardiovascular disease, cancer, espeis or a disease related to graft transplant.
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                                                                                                                                                                                                                                                                                                                                                               New enzyme polymer conjugate used for treating abnormal levels of extracellular nucleotides or platelet aggregation, graft transplant, cardiovascular disease, cancer and sepsis.
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                                                                                                             (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
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                                                                      GEN HOSPITAL
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N-PSDB; ADJ57261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New CD-39-like polypeptides and polynucleotides, useful in chromosome gene mapping, as molecular weight markers, as food supplements, or as anti-thrombotic or anti-tissue graft rejection agents.
                                                                                                     181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFR
                                                                                                                                                                LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP
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                     HOETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWI
                                                                                TINYLLGKFSOKTRWFSIVPYETNNOETFGALDLGGASTOVTFVPQNQTIESPDNALQFR
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The present invention relates to a method of treating cardiovascular disease in a subject, comprising administering an IL-17, IL-18, 4-1BB, CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists are useful for treating cardiovascular disorders, e.g. (chronic immune) myocarditis, congestive heart failure, aneurysms, angina, embolism, restenosis, ischaemia or thrombocytopenic purpura. The present sequence is a polypeptide used in the exemplification of the
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                                                                                                                                                                                                                                                                                             ADL24295 standard; protein; 510
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12-AUG-2003;
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                                         nucleotide triphosphatase; NTPase) and nucleic acid molecules encoding such polypeptides. CD39-like polynucleotides may be used as hybridisation probes. PCR primers and in chromosome and gene mapping. Polypeptides of supplements, in generating an antibody that specifically binds the polypeptide, as anti-thrombotic or anti-tissue graft rejection agents, or for regulating ATP neurotransmission in smooth muscle, peripheral ganglia or brain. Sequences of the invention are useful in modulating ecto-ATPase activity and for identifying compounds that modulate ecto-ATPase activity. The present sequence is human CD39 protein, a member of the activity. The present sequence is find sequence is the same as that shown as SEQ ID NO:13 in the sequence listing of the specification. However this sequence has additional residues at its ends.
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                                The invention relates to novel CD39-like polypeptides (CD39-like
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                                                                                                                                                                                                                                Length 510;
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100.0%; Pred. No. 5.2e-262;
ive 0; Mismatches 0;
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           8; 104pp; English.
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Matches 510; Conservative
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          Example; Fig
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The present invention relates to CD39-like polypeptide and its encoding polynucleotide. The invention is useful for preventing, treating or ameliorating autoimmune deficiency disorders including connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease or autoimmune inflammatory eye disease, myeloid or lymphoid call deficiencies, periodontal disease and other tooth repair processes, inflammatory conditions including inflammatory bowel disease and crohn's disease, leukaemias and nervous system city inflammatory conditions including inflammatory conditions and nervous system inhibiting platelet aggregation, food supplement, anti-tissue graft rejection agents, for regulating neurotransmission by ATP in smooth sequence is a human CD39 protein. Note: This sequence is stated to be the same as that shown as SEQ ID 13 in sequence listing, however these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated CD39LA polypeptide and polynucleotide, useful for preventing, treating, or ameliorating multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or graft-versus-
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autoimmune pulmonary inflammation, Guillain-Barre syndrome; autoimmune thyroiditis; insulin dependent diabetes mellitus; manatus autoimmune thyroiditis; insulin dependent diabetes mellitus; myasthenia gravis; graft-versus-host disease; alterate asthma; autoimmune inflammatory eye disease; alterate is asthma; respiratory disease; myeloid or lymphoid cell deficiency; periodontal disease; tooth repair process; inflammatory bowel disease; Crohn's disease; leukaemia; nervous system disorder; anticoagulant; food supplement; anti-tissue graft rejection; ATP neurotransmission;
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100.0%; Pred. No. 5.2e-262;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ACR) I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                47. .68
/note= "Apyrase region
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207. .228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Apyrase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JUL-2001; 2001US-00905744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00240639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chadwick BP, Frischauf A;
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                                                                                                                                                                                                                                                                                       therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-613270/59.
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                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Best Local Simi
Matches 510;
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29-JAN-1999; 99US-00240639.
13-JUL-2001; 2001US-00905589.
                                                                                                                                              WPI; 2004-613273/59
                                                                                                  NUVE-) NUVELO INC
                                                                                                                                                         GENBANK; S73813.
                                                                                                                         Chadwick BP,
                                           27-MAR-2002;
US6780977-B1
                     24-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      systemic lupus erythematosus;
human immunodeficiency virus-associated myelopathy;
transverse myelopathy; nutritional disorder; vitamin B12 deficiency;
folic acid deficiency; Wernicke disease; tobacco-alcohol amblyopia;
Marchiafava-Bignami disease; haemostatic activity; thrombolytic activity;
nutritional supplement; ecto-ATPase activity; cytostatic; immunotherapy;
                                                                                                                                                                                                     360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD39-like protein, CD39-like nucleotide triphosphatase; NTPase; cancer; leukaemia; acute lymphocytic leukaemia; acute myelocytic leukaemia; chronic leukaemia; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; Guillain-Barre syndrome; insulin dependent diabetes mellitus; myasthenia gravis; graft-versus-host disease; GVHD; allergic disorder; asthma; respiratory disorder; inflammatory disorder; septic shock; systemic inflammatory response syndrom; SIRS; Crohn's disease; central nervous system disorder; peripheral nervous system disorder; ischaemia; Parkinson's disease; Alzheimer's disease; Huntington's chorea;
               SLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQ 120
                                            HOETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWI 180
                                                                                        240
                                                                                                      300
                                                                                                                                                360
                                                                                                                                                                                                                            SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
                                                                                                                                                                                                                                        SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL 480
                                                                                                                                                                                                                                                                                      SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL 480
                                                         CTKR FEMTL PFQQFE1QG1GNYQQCHQS1LELFNTSYCPYSQCAFNG1FLPPLQGDFGAF
                                                                                                                                                                                            TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFR
                                                                                                                                   LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP
                                                                                                                                                                                                                                                                                                                   MVLFSLVLFTVAIIGLLIFHKPSYFWKDMV 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Apyrase (ACR) IV"
                                                                                                                                                                                                                                                                                                                                481 MVLFSLVLFTVAIIGLLIFHKPSYFWKDMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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/note= "Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human CD39 protein #3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; enzyme
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conclocition triphosphatase; NIPase) and their encoding polymucleotides.

The invention is useful in treating cancer, leukaemia and related disorders such as acute lymphocytic leukaemia, acute myelocytic leukaemia, acute myelocytic leukaemia, and chronic leukaemia, autoimmune disorders such as multiple sclerosis, chematoid arthritis, Guillain-Barre syndrome, insulin dependent diabetes rheumatoid arthritis, Guillain-Barre syndrome, insulin dependent diabetes wellitus, myasthenia gravis and graft-versus-host disease, allergic disorders such as actima, respiratory disorders; inflammatory disorders conduscribed as actima, respiratory disorders, inflammatory disorders conduscribed such as septic shock, systemic inflammatory response syndrome (SIRS) and crohn's disease, central and peripheral nervous system disorders such as ischaemia, Parkinson's disease, Alahaimer's disease, Huntington's chorca, systemic lupus erythematosus, human immunodeficiency virus-associated myelopathy and transverse myelopathy and utritional disorders such as vicamin B12 deficiency, folic acid deficiency, Wernicke disease, tobaccocalcon amblyopia and Marchialava-Bignami disease. The invention also has haemostatic and thrombolytic acivity. The invention acts as a cytostatic conduction and is useful in immunotherapy. The present sequence is human CD39 protein represented in the specification as being the sequence listing, however the two sequences are different.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
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New antibody or its fragment that specifically binds to CD39L3 polypeptide, useful for detecting and purifying CD39L3 polypeptide, for treating leukemia, and for detecting and preventing metastatic spread of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                  present invention provides novel CD39-like polypeptides (CD39-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQ
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Pred. No. 5.2e-262;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                          Example, Fig 8; 102pp; English.
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Best Local Similarity 100.
Matches 510; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 510 AA;
                                                                                                                  cancerous cells.
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LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKFP

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ArPase activity. The invention is useful for preventing, treating or ameliorating andical condition, e.g. multiple sclerosis, rhemmatoid arthritis, autoimmune thyroiditis, diabetes mellitus, myasthenia gravis, autoimmune inflammatory eye disease, osteoporosis, osteoarthritis, alabetement's disease, Parkinson's disease, amyotrophic lateral sclerosis, leukaemia or nervous system disorders and in gene therapy. The present sequence is the human CD39 protein. Note: This sequence is stated to be the same as that shown as SEQ ID 13 in sequence listing, however these
    markers, and as food supplements and for modulating ecto-ATPase activity
                                                                                                                                                                                                                                                                                                                                              SLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQ
                                                                                                                                                                                                                                                                                                                                                                          SLY1YKWPAEKENDTGVVHQVEECRVKGPG1SKFVQKVNE1G1YLTDCMERAREVIPRSQ
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                                                                                                                                                                                                                       Length 510;
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                      100.0%; Score 2698; DB 8;
100.0%; Pred. No. 5.2e-262;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABO84674 standard; protein; 510
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                                                                                                                                                                                                                                   Local Similarity 100.
                                                                                                                                                          sequences differ.
                                                                                                                                                                                         Sequence 510 AA;
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                                                                                                              SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL 480
                                                                                                                                                                                                                                                                                                                                                                                        CD39-like protein; gene mapping; food supplement; ecto-ATPase activity; gene therapy; multiple sclerosis; rheumatoid arthritis; autoimmune thyroiditis; diabetes mellitus; myasthenia gravis; autoimmune inflammatory eye disease; osteoporosis; osteoarthritis; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; leukaemia; nervous system disorder; neuroprotective; antiarthritic; antithymuneitic; antithamenian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a CD39-like polypeptides and the encoding polymucleotides. The CD3914 polymucleotide is useful as hybridisation probes, as primers for PCR, for chromosome or gene mapping, in the recombinant production of protein, and in generation of antisense DNA or RNA. The protein of the invention is used as molecular weight
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                                               SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL
                                                                                          SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL
                              SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated CD3914 polynucleotide, useful for preventing, treating, ameliorating multiple sclerosis, rheumatoid arthritis, diabetes, osteoporosis, Alzheimer's disease, amyotrophic lateral sclerosis, or
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207. 228
/note= "Apyrase region (ACR)
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169. .19
                                                                                                                                                                                                                                                                                                                                                             Human CD39 protein #3.
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300 360 360 360 420 480

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New isolated CD39L3 polypeptide and polynucleotide, useful for diagnosing, preventing or treating HIV, hepatitis, multiple sclerosis, systemic lupus erythematosus, arthritis, diabetes and asthma.
                                                                                                                                                                                                                                                                                                                              421 SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL
             TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFR
                                    241 LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP
                                                                                                          241 LYGKDYNVYTHSFLCYGKDQALMQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP
                                                                                                                                                            301 CTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAP
                                                                                                                                                                                   SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL
                                                                                                                                                                                                                                                                        361 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL
                                                                                                                                                                                                                                                                                                             SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL
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/note= "Apyrase region (ACR)
125. .142
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                                                                                                                                                                                                                                                                                                                                                                                                                                   contiguous nuclectides of any of the 233 polynuclectide sequences given in the specification, or its complement. The nucleic acids encode cancerassociated proteins. Also included are an expression vector comprising the above case contiguous nucleic acid cited above, a host cell comprising the above comprising the above comprising the above comprising at least no me probe a cancer-associated (CA) nucleic acid comprising at least one probe comprising at least 10 contiguous nucleotides of any of the above comprising at least 10 contiguous nucleotides of any of the above comprising for a cancer as mentioned nucleotide sequences, an isolated polypeptide (encoded within an open reading frame of a CA sequence selected from any of the 35 polynucleotide sequences as mentioned in the specification, or its plynucleotide equences as mentioned in the specification, or its plynucleotide above polypeptide, a hybridoma that produces the above monoclonal antibody, a pharmaceutical composition comprising the above monoclonal antibody, a pharmaceutical composition comprising the above antibody and a pharmaceutical excipient, a kit for detecting cancer calls (Comprising the presence or absence of cancer cells in an individual, a method for inhibiting growth of cancer cells in an individual, a method for fully comprising the above polymetric agent to cancer cells in an individual, an electronic library comprising the above polymetricy of a CA protein (CA protein (CA protein (CA) methods for detecting cancer activity of a CA protein (CA) methods for detecting cancer activity of a cancer cells in a test cell sample, a cancer detecting preventing and treating cancers and a method for inhibiting the appeal of a polypeptide in a test cell sample, a cancer the present sequence is an a method sequence. Note: The cancer the present sequence is an electronic form part of the present sequence is an electronic form part of the printed cancer is the present sequence is a human CA protein sequence. The present sequence is an electronic form par
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                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to an isolated nucleic acid comprising at least 10
                                                                                                                                                                                                                                                                                                               New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHT
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                                                                                                                                                                                                                      Malandro MS;
                                                                                                                                                                                                                                                                                                                                                                                        claim 18; seqid 698; 310pp; English
                                                , 2003US-00367094.
; 2003US-0038838.
; 2003US-00417375.
; 2003US-00461862.
; 2003US-0063431.
               17-FEB-2004; 2004WO-US004730
                                                                                                                                                                                 (SAGR-) SAGRES DISCOVERY INC
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Matches 510; Conservative
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N-PSDB; ABD32958.
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                                                                                                          13-JUN-2003;
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241 LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP 300
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Matches 510; Conserv
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                                                                                 triphosphatase; NTPase) and their corresponding polymucleotides. The invention also relates to a method for making CD30 proteins. The methods and compositions of the invention are useful for the diagnosis. prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of the CD39-11ke polypeptide, such as HIV infection, hepatitis, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, Guillain-Barre syndrome, thyroiditis, diabetes, present sequence is the human CD39 protein. Note: This sequence is present especialization as being the same as the human CD39 protein represented in SEO ID NO: 13 of the sequence listing, however the
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                                                               invention relates to CD39-like polypeptides (CD39-like nucleotide
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The invention relates to a novel pharmaceutical composition active on anglogenesis comprising an endothelial cell nucleic acid whose expression is induced by an anglogenic factor and inhibited by an angiostatic agent or its complement or fragment, a polypeptide sequence encoded by the nucleic acid or its fragment, a molecule capable of inhibiting expression of the nucleic acid or a molecule which binds to the polypeptide
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ovary hyperstimulation, psoriasis, endometriosis, restenosis, angioplasty, cicatrisation, peripheral vascular disease, hypertension, vascular inflammation, Raynaud's disease, aneurism, thrombophlebitis, ischemia, angina, myocardial infarction, chronic heart disease,
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                                                                                                       Compositions containing nucleic acid or polypeptide differentially expressed in angiogenesis are useful to diagnose, prognose and treat angiogenic disorders including tumor vascularization and heart disease.
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                                                                                                                                                                                                            Claim 7; SEQ ID NO 297; 405pp; French.
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Crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis, endometriosis associated with neovascularization, restenosis due to analopplasty, overproduction of tissue due to cicatrisation, a peripheral vascular disease, hypertension, vascular inflammation, Raynaud disease, aneurism, arterial restenosis, thrombophlebitis, ischemia, angina, myocardial infarction, chronic heart disease, cardiac congestion or macular degeneration due to age or osteoporosis. This sequence corresponds to a protein encoded by a differentially expressed DNA used in the composition of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEIILRDPCFHPGYKKVVNVSDLYKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 LYGKDYNVYTHSFLCYGKDQALMQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTKRFEMTLPFQQFE1QGIGNYQQCHQS1LELFNTSYCPYSQCAFNGIFLPPLQGDFGAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 SLLLQCYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  422 SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNTNMIPAEQPLSTPLSHSTYVFL
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100.0%; Pred. No. 5.3e-262;
ive 0; Mismatches 0;
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Matches 510, Conservative
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us-09-807-660c-2.rpr

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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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sw model protein search, using • OM protein

September 21, 2005, 15:52:40 ; Search time 25 Seconds (without alignments) 1962.822 Million cell updates/sec Run on:

Title: Perfect score:

US-09-807-660C-2 2698 1 MEDTKESNVKTFCSKNILAI......VAIIGLLIFHKPSYFWKDMV 510 Sequence:

Scoring table:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 seg seg 88 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* 1 2 6 4 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Dearrintion	Description	lymphoid cell acti	hypothetical prote			probable nucleotid	probable nucleosid	hypothetical prote	7A19.33 protein -	hypothetical prote	probable quanosine	nucleoside triphos	hypothetical prote	apyrase (EC 3.6.1.	hypothetical prote	guanosine-diphosph	nucleoside-triphos	C4-dicarboxylase-b	beta-galactosidase	hypothetical prote			м	hypothetical prote	5	TipC protein - sli	hypothetical prote	$\vec{}$	hypothetical prote	n, N-
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ALIGNMENTS

lymphoid cell activation antigen - human (5) Species: Homo sapiens (man) (5) Species: Homo sapiens (man) (5) Species: Homo sapiens (man) (5) Species: O2-Jul-1996 #sequence_revision O2-Jul-1996 #text_change O9-Jul-2004 (5) Accession: 156342 (C.R.; Delespesse, G.J.; Schoenborn, M.A.; Armitage, R.J.; Fanslow, W.C.; J. Immunol. 153, 3574-3583, 1994 (G.J.; Schoenborn, M.A.; Armitage, R.J.; Fanslow, W.C.; A; Title: The CD39 lymphoid cell activation antigen. Molecular cloning and structural ch. A; Reference number: 156242; MUID:95015846; PMID:7930580 (A; A; A; Caresion: 156242 (A; A; Caresion: 156242 (A; Caresion: 156

ö Gaps ö Length 510; 0; Indels 100.0%; Score 2698; DB 2; 100.0%; Pred. No. 4.1e-206; ative 0; Mismatches 0; Best Local Similarity 100. Matches 510; Conservative Query Match

240 300 300 SLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQ 120 61 SLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQ 120 121 HQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWI 180 180 240 360 420 9 9 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHT 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHT 121 HQETPVYLGATAGMRLIRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWI TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFR LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP 241 LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFE1QG1GNYQQCHQS1LELFNTSYCPYSQCAFNG1FLPPLQGDFGAF SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 241 61 181 301 361 셤 ò g ઠે 셤 ò g ઠે g ò ò 유 ò

480

361 SAFYFVWKFLNLTSEKVSQEKVTEMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420

SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL 480

SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL

421 421

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Query Match
Best Local Similarity 31.2%
Matches 123; Conservative
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A,Status: preliminary
A,Molecule type: DNA
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                                                                                                                                                                  hypothetical protein F7A19.34 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 (Species: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 (Species: 02-Mar-2001 Boston, D.; Conn, L.; Conway, A.B.; Conway, A.R.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Aluthors: Mature 408, 816-820, 2000 A; Authors: Hunter, J.L.; Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Southwick, A.M.; Sun, H.; Tallon, A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Accession: D86276 A.Accession: D86276 A.Accession: D86276 A.Accession: D86276 A.Accession: D86276 A.Accession: D86276 A.Accession: Balzberg, S.D. A.Accession: Balzberg, S.D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -IYDTN-SKNYSSGFLADESKLKGSLQAAGNFSKCRSATFALLKEGKENCLYEHCSIGST 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       414
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LRGYCFSAAYTISMLHDSLGIALDD-ESITYASK----AGEKHIPLDWALG 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77; Mismatches 182;
                      142; Conservative
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hypothetical protein F14L17.1 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)

RESULT 3

E86276

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Chin, C.W.; White, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R.; Theologia, A.; Ecker, J.R.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Althors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C. A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, II, A; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chronosome lof the plant Arabidopsis.
A; Reference number: A86141; WUID:21016719; PMID:11130712
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Cybecies: Saccharomyces cerevisiae
Cybecies: Saccharomyces cerevisiae
Cybecies: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
CyAccession: S50463
CyAccession: S50463
Rybietrich, F.S.
submitted to the EMBL Data Library, December 1994
Aybescription: The sequence of S. cerevisiae cosmids 9537, 9581, 9495, 9867, and lambda characterence number: S50463
AyReference number: S50463
AyReference number: S50463
AyReference number: S50463
AyReferences: UNA
AyReferences: UNA
AyReferences: UNIPROT:P40009; EMBL:U18778; NID:g603592; PID:g603597; GSPDB:GN00005, Cyfenetics:
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A;Cross-references: UNIPROT:Q9M9T7; GB:AE005172; NID:g7262666; PIDN:AAF43924.1; GSPDB:GNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 LDVTRRVLRSSGFKFQDEWATVISGTDEGIYAWVVANHALGSLG-------GDPL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 WQKLAKDIQVASNE-ILRDPCFHPGYKKVVNVSDLYKTPCTK------RFEMTLPF 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 FGL-GEK---EWLSEMILAGKRFCGEEWSKLKEKYPTTKDKYLHRYCFSSAYIISMLHDS 353
Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 ---QVQAAGDFTKCRSATLAMLQEGKENCAYKHCSIGSTFTPNIQGSFLATENFFHTSKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 PGISKFVQKVNEIGIYLIDCMERARBVIPRSQHQETPVYLGATAGMRLLRMESBELADRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 ETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGK-DYNVYTHSFLCYGKDQA---L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 QQFEIQGIGNYQQCHQSILELF--NTSYCPYSQCAFNGIFLPPLQGDFGAFSAFYFVMKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 PGLSSYADNPEGASVSVTKLVEFAKGRIPKGKLKKSDIRLMATAGMRLLDVPVQE---QI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 469.5; DB 2;
; Pred. No. 2.2e-29;
65; Mismatches 145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       427 YHFTADSWEHIHFIGKI--QGSDAGWTLG-YMLN 457
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31.2%;
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A;Cross-references: SGD:S0000807
A;Map position: 5R
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Cjaccession: G8442

K;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, ...
Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: UNIPROT:080612; GB:AE002093; NID:93461821; PIDN:AAC32915.1; GSPDB:G:
        210 GALDLGGASTQVTF-VPQNQTIESPD------NALQFRLYGKDYNVYTHSFLCYGK 258
                                                                                                                                                                                                                                          169 GFLDMGGASVQIAFELPPSQLKNYKDSISTVHIGLQNGQQL----EYPLFVTTWLGFGA 223
                                                                                                                                                                                                                                                                                          259 DQALWQKLAKDIQVASNEI---LRDPCFHPGYKKVVNVSDLYKTPCTKRFEMTLPFQQFE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 EKVSQ------EKVTEMMKKFCAQPWEEI-----KTSYAGVKEKYLSEYCFSGTY 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 DVFDMGGSYHFPNFYKKVDE----YCGTEWETMLSRLYNKELTPSTDENKLEKLCFKASW 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----YHFTADSWEHIHFIGKIQGSDAGWTLGYML 456
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                                                                                                                                                                                                                                                                                                                                                                                                 316 IQGIGNYQQCHQSILELFNTSY-CPYSQCAFNGIFLPPLQGDFGAFSAFYFVMKFLNLTS 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable nucleoside triphosphatase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                              264 FAGTGDLKQCLKLTYNLLNKDKPCSMDPCNFDGISIPPV--DF-ANTEFVGVSEFWYTTN
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                                                                                      SL-SNYPFDF----QGARIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETNNQETF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419 ILSLLLQG------
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Matches 136; Conservative
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A; Residues: 1-516 <STO>
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C;Superfami
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() Species: Schizosaccharomyces pombe
() Species: Schizosaccharomyces pombe
() Accession: T40856
R.Ramsperger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
A.Reference number: Z21952
A.Residues: DNA
A.Residues: 1-572
A.Res
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                                                                                                                                                                                                                                                                                                             151 VVERSLSNYPFDF-----QGARIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETN 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEI-----KTSYAGVKEK 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLSEYCFSGTYILSLLLQGY---HFTADSWEHIH-----FIGKIQGSDAGWTLGYML-- 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 450 ASGSILAGNDDFWVGIAPSERRTKLTGKKFIPGKLLESDQLKKQSSSLSNKGFLMWFAII 509
                                                                                                                                                               99
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                                                                                                                                    SKFVQKVNE-IGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELADRVLD
                                                                                                                                                                                                                                             205 NQETFGALDLGGASTQVTFVPQNQ------TIESPDNALQFRLYGKDYNVYTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFLCYGKDQALWQKLAKDIQVA-----SNEILRDPCFHPGYKKVVNVSDLYKT
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TWLGFGANQARRRYLAQLINTLPENTNDYENDDFSTRNLNDPCMPRG----SSTDF---
                                                                                                      NVKYGIVLDAGSSHTSLYIYKWP-----AEKENDTGV-----VHQVEECRVK-GPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCTKRFEMTLPFQQFEIQGIGNYQQCHQSILE-LFNTSYCPYSQCAFNGIFLPPLQGDF-
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        Length 630;
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                                                        Indels
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16.9%; Score 455.5; DB 2;
llarity 25.0%; Pred. No. 5.4e-28;
Conservative 103; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.1%; Score 435.5; DB 2; Best Local Similarity 26.7%; Pred. No. 1.8e-26; Matches 144; Conservative 77; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   510 CCIFY-----LİFHR 519
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                          Similarity
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                                                     139;
Query Match
Best Local S:
Matches 139
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hypothetical protein C33H5.14 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T34147
R;Bradshaw, H.; Stellyes, L.
submitted to the RMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C33H5.
A;Reference number: Z21482
A;Reference number: Z21482
A;Reference number: Z21482
A;Accession: T34147
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Besidues: 1-485 - GRA>
A;Accession: T34147
A;Gresinental source: strain Bristol N2
C;Genetics:
C;Genetics:
A;Gene: CESP:C33H5.14
A;Introns: 22/1; 8311; 120/2; 167/1; 269/3; 399/3
C;Superfamily: nucleoside triphosphatase chromatin-associated
                           250 TYNLYSHSFLHFGQNAAHDKLWGSLLSRDHNSAVEPTREKIFTDPCAPKGYNLDANTQKH 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KFCAQPWEEI-----KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHI-HFIG 441
                                                                                                                                          310 LSGLLAEESRLSDSF-----QAGGNYSQCRSAALTILQDG------NGRILIIIAG- 354
                                                                                                                                                                                          357 FGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSG 416
                                                                                                                                                                                                                                                                                     417 TYILSLILLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHST 476
                                                                                                                                                                                                                                                                                                                   ||:|||
406 AYIVSLLHDTLGIPLDD-ERIGYANQAGDIPLDWALGAFIQQTATETSQHAASGNLHWFH 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 SNEILRDPCFHPGYKKVVNVSDLYKTPCTKRFEMTLPPQQFEIQGIGNYQQCHQSILELF 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 NTS---YCPYSQCAFNGIFLPPLQ---GDFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMK 387
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DYNVYTHSFLCYGKDQA---LW-QKLAKD----IQVASNEILRDPCFHPGYKKVVNVSDL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPF 161
                                                                                                                                                                                                                       SDSNIRIIDGAMEGIYSWIAVNYILGRFDKE-------NDSKVGMIDMGGASVQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 AFEIANEK-ESYNGGNVYEINLGSIETNEDYKYKIYSTTFLGYGANEGL-KKYENSLVKS
                                                                                              297 YKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 NVKYGIVLDAGSSHTSLYIYKWPAEKENDTGV---VHQVEECRVK-GPGISKFVQKVNEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 VEYLIPLLRFÄEEHIPYEQLGEIDLLIFÄTÄGMRLLPEAQKDAIIKNLQNGLKSVTALRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 DFQGARIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQV
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                                                                                                                                                                                                                                                                                                                                                                                 477 YVF-----LMVLFSL-VLFTVAIIGLLIFHKP 502
                                                                                                                                                                                                                                                                                                                                                                                                                              465 ALFSNHPKTLHYLIGIPILMTVLVYLVTKWRKP 497
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Cipacies: Arabidopsis thaliana (mouse car cress)
Cipacies: Arabidopsis thaliana (mouse car cress)
Cipacies: Arabidopsis thaliana (mouse car cress)
Cipacies: O2-Mar-2001 #sequence_revision O2-Mar-2001 #text_change O9-Jul-2004
Cipate: O2-Mar-2001 #sequence_revision O2-Mar-2001 #text_change O9-Jul-2004
Cipacession: C86276
Cipate: O2-Mar-2001 #sequence_revision O2-Mar-2001 #text_change O9-Jul-2004
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Anthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Sun, P.; Southwick, A.M.; Sun, H.; Tallon, I A,Authors: Salzeberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Machence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: C86276
A; Accession: C86276
A; Accession: C86276
A; Accession: C86276
A; Residues: 1-508 ASTO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 GNVSYNLYSHSFLDFGQD-AAQEKLSESLYNSAANSTGEGIVPDPCIPKGYLLETNLQKD 292
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345 KYCQKDWNDIQDGFKRNEFPNADIERLGTNCFKAAWVTSVLHDG--FNVDKTKHLFQSVL 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 KENDTGVVHQVEECRVK-GPGISKFVQKVNEIGIYLIDCMERAREVIPRSQHQETPVYLG 129
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                                                                                       190 SQKTRWFSIVPYETNN-QETFGALDLG-----GASTQVTFVPQNQTIESPDNALQFRLY
                                                            442 KIQGSDAGWTLGYML-----NLTNMIPAEQPLSTPLSHSTYVFLMVLFSLVLFTVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 SKNILAILGFSSIIAVIALLAVG---LTQNKALPENVKYGIVLDAGSSHTSLYIYKWPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 TKSIIFVI-VACVTIALGLLFIGYSILRSGRNRRVSLHYSVIIDGGSSGTRVHVFGYRIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 ATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 GK-DYNVYTHSFLCYGKDQALWQKLAKDI-QVASNE----ILRDPCFHPGYKKVVNV-SD
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C;Superfamily: nucleoside triphosphatase chromatin-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 14.9%; Score 402.5; DB 2; Best Local Similarity 27.4%; Pred. No. 6.4e-24; Matches 129; Conservative 81; Mismatches 186;
                                                                                                                                                                                                                                                                    7A19.33 protein - Arabidopsis thaliana
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hypothetical protein R07E4.4 - Caenorhabditis elegans

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uncleoside triphosphatase precursor, chromatin-associated - garden pea CiSpecies: Pisum sativum (garden pea) CiState: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004 CiAccession: 865147; 848859 Fisus Mol. Biol. 30, 135-147, 1996 A;Hsich, H.L.; Tong, C.G.; Thomas, C.; Roux, S.J. Plant Mol. Biol. Biol. Biol. 30, 135-147, 1996 A;Fitle: Light-modulated abundance of an mRNA encoding a calmodulin-regulated, chromatin A;Reference number: 865141; MUID:96197404; PMID:8616230 A;Accession: 865147 A;Accession: 865147 A;Molecule type: mRNA A;Residues: 1-455 cH82> A;Residues: 1-455 cH82> A;Crose-references: UNIRROT:PS2914; EMBL:Z32743; NID:9563611; PIDN:CAA83655.1; PID:95636 C;Keywords: nucleoside triphosphatase chromatin-associated
                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278
                                                                                                                                                                                                                                                                                                                                                   KDGVSILEGSMEGIYAWITINYLLGTLGGKA-----THSTVAVMDLGGASTQLV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 FEPRFASDGESLVDGDHKYVLDYNGEQYELYQHSHLGYGLKEA--RKLIHKFVLNNAEAL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RD-----TLPFQQFEIQGIG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 KESLELLGDSTSIIHPCLH-----LNASLTHPDSKSEASEVVFVGPSLAHLSLQCRGIA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 NYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFG----AFSAFYFVMKFLNLTSE 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E-----KALYKDKNCPVRPCSFNGVHQPKFTETFTDSPIYLISYFYDRMISLGMPS- 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 KVSQEKVTEMMKKFCAQP--WEEIKTSYAGVKB-KYLSEYCFSGTYILSLLLQGYHFTAD 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 ISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELADRVLD 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVERSLSN-YPFDFQ--GARIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETNNQE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
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                                                                                                                                                                                                                                                  106 TDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSN-YPFDF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FVPQ----NQTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEIL
                                                                                                                                                                                                                      48 KYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEE--CRVKGPGISKFVQKVNEIGIYL
                                                                                                                                                                                                                                                                                                                                                                                                                       -QGARIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVT
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                                                                                                                                                                       Gaps
                                                                                                                                                                 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91;
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                                                                                                                                                                    Indela
                                                                                                                        Length
                                                                                                                  Query Match 14.1%; Score 381.5; DB 2; Best Local Similarity 27.1%; Pred. No. 3.4e-22; Matches 121; Conservative 71; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWEHIHFIGKIQGSDAGWTLGYMLNL 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --RQLHTAKKIDNKELGWCLGASLSM
                                         A;Gene: SPDB:SPAC824.08
A;Map position: 1
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     C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #text_change 20-Sep-1999
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16696
A;Accession: T16696
A;Reference number: 218561
A;Reference number: 218561
A;Reference number: 218561
A;Reference number: 218561
A;Reference number: 218566
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Redidues: 1-557 cMIL>
A;Rolecule type: DNA
A;Redidues: 1-557 cMIL>
A;Coss-references: EMBL:U39652; NID:g1049390; PID:g1049394; PIDN:AAA80403.1; CESP:R07E4
A;Coss-references: Exrain Bristol N2
C;Genetics
C;Genetics
A;Introns: 39/1; 67/1; 145/2; 192/1; 244/3; 317/3; 451/3; 488/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable guanosine-diphosphatase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39109
R;Barrell, B.G.; Rajandream, M.A.; Quail, M.; Seegar, K.; Harris, D.
Submitted to the EMBL Data Library, October 1999
A;Reference number: Z21828
A;Accession: T39109
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-556 < ABR>
A;Residues: 1-556 < ABR>
A;Cxoss-references: UNIRROT: 09UT35; EMBL:AL121741; PIDN:CABS7338.1; GSPDB:GN00066; SPDB:A;Experimental source: strain 972h-; cosmid c824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 D----TGVVHQVEECRVK-GPGISKFVOKVNEIGIYLTDCMERAREVIPRSQHQETPVYL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 ELIQIEPVIYDNKPVMKKISPGLSTFGTKPAQAAEYLRPLMELAERHIPEEKRPYTPVFI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATAGMRLLRMESEELADRVLDVVERSLSN-----YPFDFQGARIITGQEEGAYGWIT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INYLLGKFSQ-KTRWFSIVPYETNNQETFGALDLGGASTQVTF-VPQNQTIES----- 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 LGCREDDSL-FK----YKLFVITFLGYGVNEGIRKYEHMLLSKLKDQNGTVIQDDCMPL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYKKVVNVSDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFN----TSYC--P 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 NLHKTVTLEN------GENFVRRGTGNWNTCSNEVKKLLNPESSSEVCKAE 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 YSQCAFNGIFLP--PLQG-DFGAFSAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEE 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 AAKCYFGAVPAPSIPLSNIEMYGFSEYWYSTHDVLGLGGQYDAENIAKKTQQYCSKRWST 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397 I----KTSYAGVKEKYLSEYCFSGTYILSLLLQGYHFTADSWEHIHF--IGKIQGSDAG 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            406 IQAESKKOLYPRADEERLRTQCFKSAWITSVLHDG--FSVDK-THNKFQSVSTIAGQEVQ 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73
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;Species: Caenorhabditis elegans
;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
;Accession: T16696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 ILGFSSIIAVIALLAVGLTQNKALPENV-----KYGIVLDAGSSHTSLYIYKWPAEKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PDNALQFRLYGKDYNVYTHSFLCYGKDQALWQ---KLAKDIQVASNEILRDPCFHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 14.7%; Score 397; DB 2; Length 55
Best Local Similarity 25.0%; Pred. No. 2e-23;
Matches 133; Conservative 96; Mismatches 218; Indels
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110

C.B.

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A,Cross-references: EMBL:U18779; NID:g603625; PIDN:AAB65000.1; PID:g603637; MIPS:YEL042<sup>o</sup>C,Genetics:
A,Gene: SGD:GDA1
                                                                                                                                                        sphingolipid glycosylation
                                                                                                                                                                                                                                              A; Wolecule type: DNA
A; Residues: 1-518 <ABE.
A; Residues: 1-518 <ABE.
A; Residues: 1-518 <ABE.
A; Cross-references: UNIPROT: P32621; EMBL: L19560; NID: G349392; PIDN: AAA34656.1; PID: G349
A; Note: sequence extracted from NCBI backbone (NCBIN: 134708, NCBIP: 134711)
A; Molecule type: protein.
A; Residues: 125-144; 238-257; 276-281; 366-374; 399-412 <ABE.
B; Mulligan, J.T.; Dietrich, F.S.; Hennessey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor, Bubmitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: S30837
A;Molecule type: DNA
A;Redidues: 1-518 <MVL>
A;Coss-references: GB:U18779; EMBL:L10830; NID:g603625; PIDN:AAB65000.1; PID:g603637
R;Dietrich, F.S.
                                                                                         K.; Hirschberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F--DTDSVGAANSLDPLLKVAMNYVPIKARSCTPVAVKATAGLRLLGDAKSSKILSAVRD 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --TFGALDLGGASTQVTFVPQ---NQTIESPDNALQFRLYGKDYNVYTHSFLCYG---- 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --KDQALWQKLAKDIQVASNE----ILRDPCFHPGYKKVVNVSDLYKTPCTKRFEMTLP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----QGDFGA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 C;Accession: A40732; B40732; G30837; S50502 R;Abeijon, C.; Yanagisawa, K.; Mandon, E.C.; Hausler, A.; Moremen, K.; Hirsc J. Cell Biol, 122, 307-323, 1993 A;Title: Guanosine diphosphatase is required for protein and sphingolipid gl A;Reference number: A40732; MUID:93308137; PMID:8391537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSAFYFVMKFLNLTSEKVSQEKVTEMMKKFC--AQPWEEIKTSYAGVKEKYLSE--YCFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmids 8199, 8334, and
A;Reference number: S50491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416 GTYILSLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNL 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.0%; Score 322.5; DB 2; Best Local Similarity 26.6%; Pred. No. 1.5e-17; Matches 123; Conservative 72; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: SGD:S0000768; MIPS: YEL042w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: S50502
A;Molecule type: DNA
A;Residues: 1-518 <DIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 5L
C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 KENDIGVVHQVEE---CRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : |: :||: :||: ASH--GMPFKVEKEIFQEVK-PGLSSFAKSPSSAADSLEPLLQRARKEVPHFWWEKTPIT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGATAGMRLLRMESEELADRVLDVVERSLSNYPF--DFQGA-RIITGQEEGAYGWITINY 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 ---EGHHIRLFTHSFLGNGLIAARLNILQLETDNEIESTHQLITSCMPEGYQ----- 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 PVYLFSYFFDRALNSGLVKGNEGGKIELROFKEAAEIACRREKTEIDDG-----SHWMPW 387
                                                                                         LCMDLIYEYTLLVDG--FGLNPHKEITVIHDVQYKNYLVGAAWPLGCAIDLVSSTTNKI 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein KO8H10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.-1999 #sequence_revision 15-Oct.-1999 #text_change 09-Jul-2004
C;Accession: T23508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 LAILGESSIIAVIALLAVGLTQNKALPENVK----YGIVLDAGSSHTSLYIYKW---PAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 LKATAGLRLL---PGDMADDILESVEERIFNSGFFAAPPDAVNVMPGSDEGVYSWFTLNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLGK-FSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESP----DNALQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 LLETLFTDE----PTVGHKPAAHRSVAAFDLGGGSTQLTYWPNNEAVFSEHVGYERDIDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72;
                                                                                                                                                                                                                                                                                                     C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05
C; Accession: T23508
R; Gardner, A.
Submitted to the EMBL Data Library, November 1996
A; Reference number: 219750
A; Reference number: 219750
A; Reseasion: T23508
A; Reseasion: T23508
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-479 eMIL.
A; Residues: 1-470 eMIL.
A; R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.3%; Score 332; DB 2; Length 47 26.1%; Pred. No. 2.3e-18; ive 80; Mismatches 211; Indels
                                                   YCFSGTYILSLLLOGYHFTADSWEHIHFIGKIOGSD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
A40732
guanoaine-diphosphatase (EC 3.6.1.42)
N'Alternate names: protein YEL042w
C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 26.19
Matches 128, Conservative
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465 LSPQVSLLHTGYDIPLQ--RELRTGKKIANKEIGWCLGASLPL 505

Search completed: September 21, 2005, 16:21:57 Job time: 29 secs

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September 21, 2005, 13:13:33; Search time 91 Seconds (without alignments) 2869.894 Million cell updates/sec
5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
                                                                                   OM protein - protein search, using sw model
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US-09-807-660C-2 2698 1 MEDTKESNVKTFCSKNILAI......VAIIGLLIFHKPSYFWKDMV 510 1612378 segs, 512079187 residues Gapop 10.0 , Gapext 0.5 **BLOSUM62** Perfect score: Scoring table: Sequence: Searched:

1612378 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 200000000 08 08 Minimum Maximum

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P49961 homo sapien	P55772 mus musculu	Q921q6 mus musculu	Q8cdv7 mus musculu	P97687 rattus norv	Q9myu4 sus scrofa		bos	Q8cebl mus musculu	Q6dfs1 xenopus tro	Q6gp74 xenopus lae	Q6dc46 brachydanio		gallus	gallus	rattus	O55026 mus musculu	Q921rl mus musculu		P79784 gallus gall	xenopu	Q66164 brachydanio	Q7t014 brachydanio	Q6nvi9 xenopus tro		Q6uvz0 homo sapien	Q9y513 homo sapien	ratto	Q8bfw6 m mus muscu	Q6zm68 brachydanio	Q8n6k2 homo sapien
	ENP1 HUMAN	ENP1 MOUSE	<u>0</u> 921 <u>0</u> 6	Q8CDV7	ENP1 RAT	ENP1 PIG	Q86V <u>V</u> 3	ENP1_BOVIN	Q8CEB1	Q6DFS1	Q6GP74	Q6DC46	060022	ENP1_CHICK	090x <u>6</u> 6	ENP2_RAT	ENP2_MOUSE	Q921R1	06ZM69	ENP2_CHICK	Q6GNA4	Q66L64	Q7T014	OENVI9	ENP3_HUMAN	Qeuvzo	ENP2 HUMAN	Q80Z <u>2</u> 6	QBBFW6	Q6ZM68	Q8N6K2
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Q7YTA4 Q8K0L2 Q8UVX9 Q8UVX9 Q8UVX9 Q8UXB Q8UXB Q8HDB Q6XGV2 Q6FRC2 Q6FRC2 Q6HZQ Q6H3Q Q9M9T7
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698.5 629.5 511.5 511.5 110.5 499 499 499 499 486 486 486 486 486
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## ALIGNMENTS

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TISSUE=Placenta;
MEDLINE=99332082; PubMed=10405171; DOI=10.1016/S0014-5793(99)00751-6;
Mateumoto M., Sakurai Y., Kokubo T., Yagi H., Makita K., Matsui T.,
Titani K., Fujimura Y., Narita N.;
"The cDNA cloning of human placental ecto-ATP diphosphohydrolases I and II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Christoforidis S., Papamarcaki T., Galaris D., Kellner R., Tsolas O.; "Purification and properties of human placental ATP diphosphohydrolase.";
                                                                                                                                                                                           SEQUENCE OF 1-30; 49-65; 94-97; 88-93; 193-223; 245-265; 382-385 AND 399-405 (ISOFORM PLACENTAL I).
TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 240-242; 162-166; 185-189; 210-223; 243-249 AND 288-297.
TISSUE=Placenta;
MEDLINE=96096723; Pubmed=8529670;
         P49961; O9UQO9; O9X3Q;
01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
(NTPDasel) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell
activation antigen) (Ecto-apyrase) (CD39 antigen).
                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM VASCULAR).
TISSUE=Umbilical vein;
MEDLINE=97149441; PubMed=8996251;
RObson S.C., Kaczmarek K., Riggel J.B., Candinas D., Koziak K., Millan M., Hancock W.W., Bach F.H.;
"Loss of ATP diphosphohydrolase activity with endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS PLACENTAL I AND PLACENTAL II).
510 AA
PRT;
                                                                                                                                                                                                                                                                                        structural characterization.";
J. Immunol. 153:3574-3583(1994).
[2]
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J. Exp. Med. 185:153-163(1997).
[3]
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 STANDARD;
                                                                                                                                                                             NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isoid=P49961-2; Sequence=vSP_003607;

Name=Placental II;

Name=Placental II;

Isoid=P49961-3; Sequence=vSP_003607, VSP_003608, VSP_003609;

TISSUE SPECIFICITY: Expressed primarily on activated lymphoid or and specific pressed in endothelial tissues. The vascular isoform and the placental isoform II are present in both placenta and umbilical vein, whereas placental isoform I is present in placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koziak K., Kaczmarek E., Kittel A., Sevigny J., Blusztajn J.K.,
Schulte Am Esch J. II, Imai M., Guckelberger O., Goepfert C., Qawi I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleotics to regulate purinergic neurotransmission. Could also be implicated in the prevention of platelet aggregation. Could also Hydrolyzes ATP and ADP equally well.

CATALYTIC ACTIVITY: ATP + 2 H(2)O = AMP + 2 phosphate.

COFACTOR: Requires calcium and magnesium.

SUBUNIT: Homodimer; disulfide-linked (By similarity).

ALTERNATIVE PRODUCTS:
                               Makita K., Shimoyama T., Sakurai Y., Yagi H., Matsumoto M., Narita N Sakamoto Y., Saito S., Ikeda Y., Suzuki M., Titani K., Fujimura Y.; "Placental ecto-ATP diphosphohydrolase: its structural feature distinct from CD39, localization and inhibition on shear-induced Int. J. Hematol. 68:297-310(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Palmitoylation targets CD39/endothelial ATP diphosphohydrolase to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: The N-terminus is blocked.
MISCELLANEOUS: Optimal pH is 7.0-7.5 with ATP as substrate and 7.5-8.0 with ADP.
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116; Kaczmarek E., Koziak K., Sevigny J., Siegel J.B., Anrather J., Beaudoin A.R., Bach F.H., Robson S.C.; "Identification and characterization of CD39/vascular ATP diphosphohydrolase."; J. Biol. Chem. 271:33116-33122(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96215267; PubMed=8626624; DOI=10.1074/jbc.271.17.10391; Wang T.F., Guidotti G.; "CD391san ecto-(CG24,Mg7+)-apyrase."; US199 is an ecto-(C324,Mg7+)-apyrase."; J. Biol. Chem. 271:9898-9901(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PALMITOYLATION.
MEDLINE=20102721; PubMed=10636909; DOI=10.1074/jbc.275.3.2057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caveolae.";
J. Biol. Chem. 275:2057-2062(2000).
-!- FUNCTION: In the nervous system, could hydrolyze ATP and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the GDA1 / CD39 NTPase family. DATABASE: NAME=PROW, NOTE=CD guide CD39 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd39.htm".
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Name=Placental 1;
MEDLINE=99062444; PubMed=9846014;
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                                                                                                                                                                                                                                                                            Cytoplasmic (Potential).

N-linked (GlCNAc. .) (Potential).

I and isoform Placental II).
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PFTSAPPAPTSCCFLFQIQ (in isoform Placental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQ
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GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0007596; P:blood coagulation; TAS.
InterPro; IPR000407; GDA1_CD39_NTPASE.
Pfam; PF01150; GDA1_CD39_1.
PROSTE; PS01238; GDA1_CD39_NTPASE; 1.
Alternative splicing; Antigen; Calcium; Direct protein sequencing;
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Missing (In isoform Placental II).
/FTId=VSP 003609.
SS -> G (In Ref. 5).
D -> K (in Ref. 4).
T -> TGET (in Ref. 5).
V -> Y (in Ref. 5).
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                                                                                                                                           Glycoprotein; Hydrolase; Lipoprotein; Magnesium; Palmitate;
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Extracellular (Potential)
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EMBL, 873813; AAB32152.1; -.
EMBL, 1087967; AAB47722.1; -.
EMBL, AJ133133; CAB41886.1; -.
EMBL, AJ133134; CAB41887.1; -.

PIR; 156242; 156242. Genew; HGNC:3363; ENTPD1. MIM; 601752; -.

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(See http://www.isb-sib.ch/announce/
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GO; GO: 0006200; P. ATP catabolism; IDA.
GO; GO: 00062186; P. P.-G-protein coupled receptor protein signalin. . .;
GO; GO: 0003186; P. Pidatelet activation; IDA.
GO; GO: 0003181; P. Pipatne ribonucleoside diphosphate catabolism; IDA.
InterPro; IPR000407; GDA1_CD39_NTPase.
Pfam; PF01150; GDA1_CD39; I.
PROSITE; PS01238; GDA1_CD39_NTPASE; I.
Antigen; Calcium; Glycoprotein; Hydrolase; Magnesium; Transmembrane.
DOMAIN
                                                                                                                                                                                        MEDINE=95015846; PubMed=7930580; Maliazewski C.R., Delespesse G.J.T., Schoenborn M.A., Armitage R.J. Fanslow W.C., Nakajima T., Baker E., Sutherland G.R., Poindexter K. Birks C., Alpert A., Friend D., Gimpel S.D., Gayle R.B. III; "The CD39 lymphoid cell activation antigen. Molecular cloning and
                                                                                                                                                                                                                                                                                                                               an
                                       our-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
activation antigen) (Ecto-APP diphosphohydrolase) (ATPDase)
Name=Entpdl; Synonyms=Cd39;
Mus musculus (Mouse)
                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                    STRAIN=129/SvJ;
MEDLINE=9839871; PubMed=9730622;
Schoenborn M.A., Jenkins N.A., Copeland N.G., Gilbert D.J.,
Schoenborn Maliazewski C.R.;
"Gayle R.B. III, Maliazewski C.R.;
"Gene structure and chromosome location of mouse Cd39 coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the Buropean Bioinformatics Institute. There were by non-profit institutions as long a modified and this statement is not removed. entities a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:102805; Entpd1.
GO:0005605; C:basal lamina; IDA.
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                                                                                                                                                                                                                                              structural characterization.";
                                      STANDARD;
                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                             NCBI_TaxID=10090;
                                      ENP1 MOUSE
P55772;
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EMBL;
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STRAIN-CZECH II; TISSUE-Mammary tumor;
MEDLINE-2238625; PubMed=1247932; DOI=10.1073/pnas.242603899;
MEDLINE-2238825; PubMed=124.7932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                    Cycoplasmic (Potential).
N-linked (GlcNAc. .) (Potential).
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                                                                                                                                                                                                                              Length 510;
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                    Extracellular (Potential).
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Last annotation update)
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Pred. No. 5.4e-150;
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53; Mismatches
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Matches 389; Conservative
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Name=Entpdl;
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Statcheron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McRwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willahon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Redriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield X.S., Xryunski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Tu Generation and initial analysis of more than 15,000 full-length human an ouse CDNA sequences.
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; MGI:102805; Entpd1.
GO:0005605; C:bacal lamina; IDA.
GO:0016021; C:integral commbrane; TAS.
GO:0004650; F:apyrase activity; IDA.
GO:000180; P:ATP catabolism; IDA.
GO:000186; P:ATP catabolism; IDA.
GO:000186; P:platelet activation; IDA.
GO:000181; P:putine ribonucleoside diphosphate catabolism; IDA.
GO:000181; P:putine ribonucleoside diphosphate ratabolism; IDA.
m; PF01150; GDA1_CD39; 1.
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Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011278; AAAH11278.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS01238; GDAI_CD39 NTPASE; 1.
510 AA; 57176 WW; E77BB644AE1413A0 CRC64;
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=2059013; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
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STRANIE-STBL/637 IISSUE-Testis;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I and I annotation of "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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STRAIN=C57BL/6J; TISSUB=Testis;
STRAIN=C57BL/6J; TISSUB=Testis;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hangaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CSTBL/60; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4921511C05 product:ectonucleoside triphosphate
diphosphohydrolase 1, full insert sequence.
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STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
510
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Meth. Enzymol. 303:19-44(1999).
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479 GLMVLFSLLLVAVAITGLFIYSKPSYFWKEAV
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01-MAR-2003
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Chordata; Craniata; Vertebrata; Euteleostomi;

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Eukaryota; Metazoa;
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             SO THE THE THE THE TREE BREAK 
Salto R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tamaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMEL/GenBank/DDBJ databases.
BMB1, AK029512; BAC26486.1;
MG1:102805; Entpdl.
RMG1:102805; Entpdl.
RMG2; GO:0005605; C:basal lamina; IDA.
GO: GO:0005605; C:basal lamina; IDA.
GO: GO:0005605; C:basal lamina; IDA.
GO: GO:0007186; P:ATP catabolism; IDA.
GO: GO:000181; P:Purine ribonucleoside diphosphate catabolism; IDA.
RG: GO:0000181; P:purine ribonucleoside diphosphate catabolism; IDA.
RG: GO:0000181; P:purine ribonucleoside diphosphate catabolism; IDA.
RG: GO:0000181; P:Purine ribonucleoside diphosphate catabolism; IDA.
REPEM: PF01150; GDA1_CD39_NTPase.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2010 (Rel. 45, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
(NTPDasel) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cactivation antigen) (Ecto-apyrase) (CD39 antigen).
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STRAIN-Wistar; TISSUE-Cochlea;
MEDLINE-20050856; Pubmed-10581401; DOI=10.1016/S0169-328X(99)00244-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuropharmacology 36:1189-1200(1997).

-I-FUNCTION: In the nervous system, could hydrolyze ATP and other nucleotides to regulate purinergic neurotransmission. Could also be implicated in the prevention of platelet aggregation. Hydrolyzes ATP and ADP equally well.

-I-CATALYTIC ACTIVITY: ATP + 2 H(2)0 = AWP + 2 phosphate.

-I-CATALYTIC ACTIVITY: ATP + 2 H(2)0 = AWP + 2 phosphate.

-I-SUBUNIT: Homodimer; disulfide-linked (By similarity).

-I-SUBCLIULAR LOCATION: Integral membrane protein (Potential).

-I-TSSUE SPECIFICITY: Expressed in primary neurons and astrocytes, kidney, liver, muscle, thymus, lung and spleen.

-I-FTM: N-G-Lycosylated.

-I-SIMILARITY: Belongs to the GDA1 / CD39 NTPase family.
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley; TISSUE=Brain;
MEDLINE=98031057; Pubbed=9364474; DOZ=10.1016/S0028-3908(97)00115-9;
KGGPL B., Braun N., Heine P., Maliazewaki C.R., Zimmermann H.;
"An ecto-ATPase and an ecto-ATP diphosphohydrolase are expressed in
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                                                                                                                                                                                                                                                                                                          Wang T.-F., Rosenberg P.A., Guidotti G.; "Characterization of brain ecto-apyrase: evidence for only one ecto-
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"Evidence for alternative splicing of ecto-ATPase associated with
termination of purinergic transmission.";
Brain Res. Mol. Brain Res. 73:85-92(1999).
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Potential.

Cytoplasmic (Potential).

N-linked (GlCNAc. .) (Potenlinked (GlCNAc. .) (Potenlin
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                                                                                                                                                                                                        STRAIN-Sprague-Dawley; TISSUE-Brain, and Hippocampus; PubMed=9221928;
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74.2%; Pred. No. 4.5e-147;
iive 58; Mismatches 71;
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                                                                                                                                                        AND CHARACTERIZATION
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SEQUENCE OF 432-511 FROM N.A.
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Matches 380; Conservative
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                                                                                                                                                        SEQUENCE FROM N.A.,
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                     1 MEDIKOSKVKRPCSKNILLILGFSSSVLAVIALIAVGLTHNKPLPENVKYGIVLDAGSSHT
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MEDLINE=97115856; PubMed=8955160; DOI=10.1074/jbc.271.51.33116;
Kaczmarek E., Koziak K., Sevigny J., Siegel J.B., Anrather J.,
Reaudoin A.R., Bach F.H., Robson S.C.;
"Identification and characterization of CD39/vascular ATP
diphosphohydrolase.";
J. Biol. Chem. 271:33116-33122(196).
J. Biol. Chem. 271:33116-33122(196).
rucleotides to regulate purinergic neurotransmission. Could also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sevigny J.; "Distribution, cloning, and characterization of porcine nucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 44, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
(NTPDasel) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell activation antigen) (Ecto-apyrase) (CD39 antigen).
Name-ENTPD1; Synonyms-CD39;
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Eur. J. Biochem. 267:4106-4114(2000)
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TISSUE=Aortic endothelium;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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InterPro; IPR00407; GDA1_CD39_NTPase.
Pfam, PF01150; GDA1_CD39; IPR0507:
PROSTE; PS01238; GDA1_CD39 NTPASE; 1.
Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
2; Gaps
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Potential.
Extracellular (Potential).
Potential.
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82F86869040D7735 CRC64;
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(GlcNAc. . .)
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N-linked (GlcNAc. .)
N-linked (GlcNAc. .)
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Matches 368; Conservative
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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  61 VPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLCYGK 120
                                                                     181 IGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVS
                                                                                                                                                                                                                                                               QEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLLLGGYHFTADSWEHIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                       319 IGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEKVS
                                                                                                                                                                                                                                  QEKVTEMMKKPCAQPWEE1KTSYAGVKEKYLSEYCPSGTY1LSLLLQGYHPTADSWEH1H
                                                                                                                                                                                                                                                                                                                            FIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFLMVLFSLVLFTVAIIGLLI
                                                                                                                                                                                                                                                                                                                                                      FIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFLMVLFSLVLFTVAIIGLLI
                                                DQALWQKLAKD1QVASNE1LRDPCFHPGYKKVVNVSDLYKTPCTKRFEMTLPFQQFE1QG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-0CT-2001 (Rel. 40, Last sequence update)
5-5UL-2004 (Rel. 44, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
(NTPDasel) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell
activation antigen) (CD39 antigen) (Ecto-apyrase).

Name-ENTPD1; Synonyma=CD39;
Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bovines; Bovines: Bovin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIJINE=97115858; PubMed=8955160; DOI=10.1074/jbc.271.51.33116; Kaczmarek E., Koziak K., Sevigny J., Siegel J.B., Anrather J., Beaudoin A.R., Bach F.H., Robson S.C.; "Identification and characterization of CD39/vascular ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 97-103; 123-133; 136-140; 145-168 AND 459-471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Aortic endothelium;
Chang A.S., Garcia R.L., Chang S.M., Schilling W.P.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       513 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 40, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                       510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                       FHKPSY FWKDMV
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RA Straubborg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.R., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.R., Bhar N.K.,
RA Hopkins R.F., Jordan H., Moore T., Mang J., Hsieh F.,
RA Bigleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Rapleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Rapleton M.S., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Gones S.J., Marra M.A.;
"Green Father C., Marra M.A.;
"Green E. Hondon and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                          CTRRFLTSLPFPELEIQGTGDFQKCQQSIRPLFNTSYCPYSRCSFDGVFLPLPQGDFAAF 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 VPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLCYGK 258
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                                                                                                                                    LSLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVF
                                                                     1 MESEELADRULDVVERSLSNYPPDFQGARITTGQEEGAYGWITINYLLGKFSQKTRWFSI
                                             SAFYFVMKFLNLTSEKVS-QEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC047664; AAH47664.1; -.
GO; GO:0016787; F:hydrolase activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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0
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                                                                                                                                                                                                                                                        372 AA
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Matches 372; Conservative 0; Mismatches
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Pfam; PF01150; GDA1_CD39; 1.
PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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musculus (Mouse)
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                                                                                                                                                                             SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                       SEQUENCE FROM N.A.
                                         NCBI_TaxID=10090;
   SLYIYRWPAEKENDTGVVTQIEESNVKGPGISGFAKKVNEINVYLTACMERAQKVIPSIQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTKRFEMT --- LPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDF 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAFSAFYFVMKFLNLTSEK-VSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYILSLLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHST 476
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                                                                                                                                                                                                                                                                                                                                                                                           1 MEDIKESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHT
Pfam; PF01150; GDA1_CD39; 1.
PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
library, clone:4732419M16 product:ectonucleoside triphosphate
diphosphohydrolase 1, full insert sequence. (Fragment).
                                                                                                                                                 (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                     (Potential)
                                                                                                                                                                                                                                                                                                                  DB 1; Length 513;
                                                                                                                                                                                                                                                                                                                                              72; Indels
                                                                                                                                                                                                                                                                                     20FE98F27B6D2F96 CRC64;
                                                                                     Extracellular (Potential) Potential.
                                                                                                                  Cytoplasmic (Potential).
N-linked (GlCNAc. .) (EN - Linked (GLCNAC. .) 
                                                                                                                                                                                                                                         K -> N (in Ref. 2).
INV -> CGF (in Ref. 2).
K -> V (in Ref. 2).
                                                             Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                70.8%; Pred. No. 2.1e-141; ive 73; Mismatches 72;
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                                                                                                                                                                                                                                                                                      58113 MW;
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les 364; Conservative
                                                Magnesium; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                             464
513 AA;
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482
503
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307
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101
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CARBOHYD
CARBOHYD
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CARBOHYD
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                                                                           TRANSMEM
                                                                                                       TRANSMEM
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                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                    CARBOHYD
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Matches
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
MGC80631 protein.
                                                                                                                                            CDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity ....
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                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                          TISSUE=Embryo;
                                                                                                                                            and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359
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Matches
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                                                                                                                                                                                                                                                                                                                          61 AVSTSLKSYPFDFQGAKIITGQEGGAYGWITINYLLGRFTQRGSWLSLIS-DSQKQETFG 119
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                                                                                                                                                                                                                                            ELFNTSYCPYSQCAFNGIFLPPLQGDFGAFSAFYFVMKFLNLTSEK--VSQEKVTEMMKK
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Pubmed=1247932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M. Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                     151 VVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETNNQETFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 QVASNEILRDPCFHPGYKKVVNVSDLYKTPCTKRFEMTLPFQQFEIQGIGNYQQCHQSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQKLAKDI
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Sukaryota, Metazota, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                            Length 420;
                                                                                                                                                                                Indels
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420 AA; 47261 MW; 1369E747CD4B9CE7 CRC64;
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Last annotation update)
                                                                                                                                        62.8%; Score 1693; DB 2;
ilarity 73.9%; Pred. No. 1.3e-119;
Conservative 46; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508 AA
interPro; IPR000407; GDA1_CD39_NTPase.
Pfam; PF01150; GDA1_CD39; 1.
                                   PROSITE, PS01238; GDA1_CD39_NTPASE;
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
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Name=entpdl-prov;
                                                                                                                                                         Local Similarity
hes 312; Conserv
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Matches
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06DFS1
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AC 06DFS
AC 06DFS
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SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL 480 Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human SLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNBIGIYLTDCMERAREVIPRSQ 1 MEDTKESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHT 121 HQETPVYLGATAGMRLLRMESEELADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWI TINYLLGKFSOKTRWFSIVPYETNNOETFGALDLGGASTOVTFVPONOTIESPDNALOFR LYGKDYNVYTHSFLCYGKDQALWQKLAKDIQVASNEILRDPCFHPGYKKVVNVSDLYKTP CTKRFEMTLPFQQFE1QG1GNYQQCHQS1LELFNTSYCPYSQCAFNG1FLPPLQGDFGAF SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL Gарв Xenopus laevis (African clawed frog). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 5 Length 508; Indels databases Created) Last sequence update) Last annotation update) Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) 57.5%; Score 1552; DB 2; 55.9%; Pred. No. 7.9e-109; tive 92; Mismatches 131;

240 180

300

360

420 418

120 120 180

us-09-807-660c-2.rup

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25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
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Matches 264; Conservative
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Name=zgc:100819;
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NCBI_TaxID=7955;
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Altschul S.F., Zeeberg B. A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

An Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Murny D.M., Sodergen E.J., Lu X., Glibbs R.A.,

Rahe J., Helton B., Ketteman M., Madan A., Sodiiques S., Sanchez A.,

Blakesley R. W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Nyers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

" Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                      TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
    Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.7%; Score 1530; DB 2; Length 5
55.3%; Pred. No. 3.7e-107;
ive 89; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Spieen;
Klein S., Gerhard D.S.;
Submitted (UNA-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073267; AAH73267.1; --
GO; GO: 0016787; F: hydroclase activity; IEA.
InterPro; IPR0000407; GDAl_CD39_NTPASE.
Pfam; PF01150; GDAl_CD39; 1.
PROSITE; PS01238; GDAl_CD39_NTPASE; 1.
PROSITE; PS01238; GDAl_CD39_NTPASE; 1.
                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                               cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282; Conservative
                  Xenopodinae; Xenopus
NCBL_TaxID=8355;
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RX STRAIN-Singapore local strain; TISSUB-Embryo;

RX Straubberg RL, Feingold E.A., Grouse L.H., Derge J.G.,

RA Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Barcow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Barcow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Holton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rah Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Mones S.J., Marra M.A.;

R Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                       480
                                                                                                                                                                               3 STEEFCYGENSENWNDIRFLGKIKDSDAGWTLGYMLNLTNMIPAELPYSPPLSHATYTGL 478
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                                    6 ESNVKTFCSKNILAILGFSSIIAVIALLAVGLTQNKALPENVKYGIVLDAGSSHTSLYIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EVKVKNPWHRPVVIFLMAVVAVGIVIMVSISVVQHKPLPQKYKXGIVLDAGSSHTSVFIY
361 SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL
                                                                                                                                       SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Actinopterygii, Neopterygii; Teleostei, Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.9%; Score 1373.5; DB 2; Length
52.8%; Pred. No. 2.5e-95;
ive 82; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120; GUAL CL33; 1.
492.38; GESOT NW; B789AB6DFCGA032B CRC64;
492.AA; 55507 NW; B789AB6DFCGA032B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Singapore local strain; TISSUE=Embryo;
Director MGC Project;
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                                                                                                                                                                                                                                                                                  MVLFSLVLFTVAIIGLLIFHKPSYFWKDMV 510
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GO, GO:0016787; F:hydrolase activity; IEA
GO:preserved property; FR004047; GDA_CD39_NTPase.
Pfam, PPO1150; GDA1_CD39_NTPASE; 1.
PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
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304 297 363 357 423 415

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LQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFLMVL 483
 HSFLCYGKDQALWQKLAK-----DIQVASNEILRDPCFHPGYKKVVNVSDLYKTPCTKR
                                                                                                                                                                                                  298 IDSLNHTQNLTVEGTGDPGNCVVALRSLFNFSSCKGGKDCAFNGIYQPPVHGQFYAFSNF
                                                            QKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYT
                                                                                                                                                                                 305 FEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCP-YSQCAFNGIFLPPLQGDFGAFSAF
                                                                                                                                                                                                                                            YFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Gallíformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gromach ecto-apyrase.";
J. Biol. Chem. 272:23645-23652(1997).
I. Biol. Chem. 272:23645-23652(1997).
I. Biol. Chem. 272:23645-23652(1997).
I. Biol. Chem. 272:23645-23652(1997).
I. Chem. 272:23645-23652(1997).
I. Color and the prevention of platelet aggregation.
I. Hydrolyzes ATP and ADP equally well (By shimilarity).
I. COPACTOR: Requires calcium and magnesium (By similarity).
I. COPACTOR: Requires calcium and magnesium (By similarity).
I. SUBUNIT: Homodimner, disulfide-linked (Probable).
I. SUBCELLUAR LOCATION: Integral membrane protein (Potential).
I. PTM: N-glycosylated.
I. SIMILARITY: Belongs to the GDAI / CD39 NTPase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Stomach;
MEDLINE-97442428; PubMed-9295305; DOI-10.1074/jbc.272.38.23645;
MEDLINE-97442428; T.L.; Kirley T.L.;
"Immunolocalization of the ecto-ATPase and ecto-apyrase in chicken gizzard and stomach. Purification and N-terminal sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Oviduct;
MEDLINE=98298108; PubMed=9632655; DOI=10.1074/jbc.273.26.16043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5)
(NTPDasel) (Ecto-ATP diphosphohydrolase) (ATPDasel) (Lymphoid activation antigen) (Ecto-apyrase) (CD39 antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 1-21 AND 150-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagy A.K., Knowles A.F., Nagami G.T.;
"Molecular cloning of the chicken oviduct ecto-ATP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       493 AA
                                                                                                                                                                                                                                                                                                                                                              FSLVLFTVALIGLLIFHKPSYFW 506
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                                                                                                                                                                                                                                                                                                                                                                                            FA-VLTLVAILGAAAI---QIFW 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40, Created)
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Gallus gallus (Chicken)
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                                                                                                                                                                                                                                                                                                   AFYPVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYILS 421
                                                                                                                                                                                                                                                                                                                   LLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNWIPAEQPLSTPLSHSTYVFLM 481
                                                                                                                                                                                                                                                                                                                                                                            TKRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFLPPLQGDFGAFS 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIGVVSQALTCQIEGPGISSYTSDPTQAGESLKSCLEEALALIPQAQHPETPTFLGSTAG 127
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                 YNVYTHSFLCYGKDQALWQKLAKDIQVASNE----ILRDPCFHPGYKKVVNVSDLYKTPC
                                                                                                                                                                                                  186 LGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKD
                                                         VYLGATAGMRLLRMESEELADRVLDVVERSLSNYPPDFQGARIITGQEEGAYGWITINYL
KWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETP
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Liver;
Bigonnesse F., Levesque S.A., Kukulski F., Lecka J., Robson S.C., Fernandes M.J.G., Sevigny J.;
Fernandes M.J.G., Sevigny J.;
Submitted (AuG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, A7364442; AAQ84519.1;
GO, GO:0004050; Frapyrase activity; IEA.
GO; GO:0016787; Frapyrase activity; IEA.
InterPro; IPR000407; GDA1_CD39_NTPase.
InterPro; IPR000407; GDA1_CD39_NTPase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Nucleoside triphosphate diphosphohydrolase-8 (EC 3.6.1.5)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.4%; Score 1063.5; DB 45.1%; Pred. No. 7.1e-72
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Mus musculus
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                 InterPro; IPR000407; GDA1_CD39_NTPase.
Pfam; PF01150; GDA1_CD39; 1.
PROSITE; PS01238; GDA1_CD39_NTPASE; 1.
Antigen; Calcium; Direct protein sequencing; Glycoprotein; Hydrolase;
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54034 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 PAGKW-----EHPONTEVLGALDLGGASTQITFQP-GVTIEDKNTSVLFRLYGTNYSLYT
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                                                                                                                                                                                                                                                                                                         Gallus gallūs (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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MEDLINE-21982040; PubMed=11985621;
Knowles A.F., Nagy A.K., Strobel R.S., Wu-Weis M.;
Knowles A.F., Nagy A.K., Strobel R.S., Wu-Weis M.;
Knowles A.F., Nagy A.K., Strobel R.S., Wu-Weis M.;
Enicken liver ecto-ATP-diphosphohydrolase.";
Enic J. Biochem. 269:2373-2382(2002).
EMBL; AP426405; AAL25086.1;
EGG; GO:0004505; F:Apyrase activity; IEA.
GO; GO:0016787; F:Apyrase activity; IEA.
PFem; PF01150; GDA1_CD39; 1.
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Last annotation update)
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Search completed: September 21, 2005, 16:21:24 Job time: 94 8ec8

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; OTHER INFORMATION: Description of Unknown Organism: unknown
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Patent No. 6287837

GRUERAL INPORMATION

APPLICANT: BENUDOIN, Adrien R.

APPLICANT: SEVIGNY, Jean

TITLE OF INVENTION: ATP-DIPHOSPHOHYDROLASES, PRODUCING THEI

TITLE OF INVENTION: TECHNOLOGY

TITLE OF INVENTION: TECHNOLOGY

FILE REFERENCE: ATP-DIPHOSPHOHYDROLASES-BEAUDOIN

CURRENT APPLICATION NUMBER: US/08/930,921B

CURRENT FILING DATE: 1998-01-02

BARLIER APPLICATION NUMBER: PCT/CA96/00223

EARLIER APPLICATION NUMBER: PCT/CA96/00223

SAFLING DATE: 1996-04-10

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.0
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US-10-107-576-14
US-09-905-743B-14
US-09-240-639-18
US-09-305-744B-15
US-09-905-744B-15
US-10-107-576-15
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US-09-129-112-2
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                                       61 SLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQKVNEIGIXLTDCMERAREVIPRSQ
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APPLICANT: Ford, John
APPLICANT: Ford, John
APPLICANT: Wulero, Julio
APPLICANT: Weing, George
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 28110/36457
CURRENT APPLICATION NUMBER: US/09/557,800C
CURRENT FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-00-11
PRIOR PLING DATE: 1999-00-16
PRIOR PLING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/37047
PRIOR PLING DATE: 1999-07-09
PRIOR PLING DATE: 1999-07-04
PRIOR PLING DATE: 1999-07-06
PRIOR PLING DATE: 1999-07-06
PRIOR PLING DATE: 1999-07-06
PRIOR PLING DATE: 1999-07-06
PRIOR PRIOR PLING DATE: 1999-07-16
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98.2%; Score 2650; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 7e-272;
Matches 502; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                        481 MVLFSLVLFTVAIIGLLIFHKPSYFWKDMV 510
                                                                                                                                                                                                                                                                                     481 MYLFSLVLFTVAIIGLLIFHKPSYFWKDMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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| Sequence 1, Application US/09781796C
| Patent No. 6800284
| GENERAL INFORMATION:
| APPLICANT: BEAUDOIN, Adrien R.
| APPLICANT: BEAUDOIN, Jean
| APPLICANT: BACH, Fritz H.
| APPLICANT: ROBSON, Simon
| TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT:
| TITLE OF INVENTION: TECHNOLOGY |
| FILE REFERENCE: 92033, 90019 |
| CURRENT FILING DATE: 1090-02-12 |
| PRIOR FILING DATE: 1095-04-10 |
| PRIOR FILING DATE: 1996-04-10 |
| PRIOR FILING DATE: 1996-04-10 |
| PRIOR FILING DATE: 1996-02-01 |
| PRIOR FILING DATE: 1998-02-01 |
| PRIOR FILING DATE: 1998-02-01 |
| NUMBER OF SEQ ID NOS: 8 |
| SOFTWARE: PatentIn Ver: 2.1 |
| SEQ ID NO ID NO ID NO IS |
| SEC ID NO ID N
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                                                                                                  SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL
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                                                                                                                                                                                                                                                                                                                                                       MVLFSLVLFTVAIIGLLIFHKPSYFWKDMV 510
                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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SAFYFVMKFLNLTSEKVSQEKVTEMMKKFCAQPWEEIKTSYAGVKEKYLSEYCFSGTYIL 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 43.4%; Score 1171.5; DB 4 Best Local Similarity 50.3%; Pred. No. 1.9e-115; Matches 254; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486 LVLFTVAIIGLLIFHKPSYFWKDMV 510
                                                                                                               MVLFSLVLFTVAIIGLLIFHKP 502
                                                                                                                                   ORGANISM: Human
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US-09-949-016-7977
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Sequence 38 Application US/09370625A

Patent No. 660032

GENERAL INFORMATION:

APPLICANT: Ford, John

APPLICANT: Mulero, Julio

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES

CURRENT APPLICATION NUMBER: US/09/370,625A

CURRENT FILING DATE: 1999-08-09

PRIOR PPLIANG DATE: 1999-07-16

PRIOR APPLICATION NUMBER: 09/350,836

PRIOR APPLICATION NUMBER: 09/350,836

PRIOR APPLICATION NUMBER: 09/373,447

PRIOR APPLICATION NUMBER: 09/273,447

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                                                                                                                                                                      SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL 480
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98.2%; Score 2650; DB 4;
Best Local Similarity 100.0%; Pred. No. 7e-272;
Matches 502; Conservative 0; Mismatches 0;
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US-09-370-625A-38
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US-09-370-625A-38
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LENGTH: 529
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Patent No. 6759214
GENERAL INFORMATION:
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES
TITLE OF INVENTION: ACIDS
FILE REFERENCE: 28110/36120E
CURRENT APPLICATION NUMBER: US/09/908,510A
CURRENT FILING DATE: 2001-07-13
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39.8%; Pred. No. 1.1e-90;
tive 90; Mismatches 186;
                                                                                             Sequence 4, Application US/09240639
Fatent No. 6350447
GENERAL INFORMATION.
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna-Maria
ITILE OF INVENTION: METHODS AND COMPOSITIONS REL
ITILE OF INVENTION: METHODS AND NUCLEIC ACI
FILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/09/240,639
CURRENT PRILIG DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
LENGTH: 529
Best Local Similarity 39.89
Matches 191; Conservative
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US-09-908-510A-4
                                                                    RESULT 6
US-09-240-639-4
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APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND 1TITLE OF INVENTION: ACIDS
FILE REFERENCE: 28110/36120A
CURRENT APPLICATION NUMBER: US/09/905,744B
CURRENT APPLICATION NUMBER: 09/240,639
PRIOR FILING DATE: 1999-01-29
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Best Local Similarity 39.8%; Pred. No. 1.1e-90;
Matches 191; Conservative 90; Mismatches 186;
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PRIOR APPLICATION NUMBER: 09/240,639
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 529
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ORGANISM: Homo Sapiens
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US-09-908-510A-4
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Query Match
Best Local Similarity 39.8%
Matches 191; Conservative
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US-10-107-576-4
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                                                                      ADRVLDVVERSLSNYPFDFQGARIITGQEEGAYGWITINYLLGKFSQKTRWFSIVPYETN 204
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| Sequence 4, Application US/10107660
| Patent No. 6780977
| GENERAL INFORMATION
| APPLICANT: Chadwick, Brian Paul
| APPLICANT: Chadwick, Brian Paul
| APPLICANT: Prischauf, Anna-Maria
| TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
| TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
| FILE REFERENCE: 9598-066
| CURRENT APPLICATION NUMBER: US/10/107,660
| CURRENT APPLICATION NUMBER: US/09/240,639
| PRIOR PILING DATE: 1998-01-29
| NUMBER OF SEQ ID NOS: 29
| SOFTWARE: Patentin Ver: 2.0
| SEQ ID NO 4
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ORGANISM: Homo sapiens
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US-10-107-660-4
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Sequence 4, Application US/10107576

Patent No. 6783959

GENERAL INFORMATION:
APPLICANT: Chadwick, Brian Paul
APPLICANT: Charles And Compositions Relating TO CD39-LIKE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS
FILE REFERENCE: 20110/36120H
CURRENT APPLICATION NUMBER: US/10/107,576
CURRENT APPLICATION NUMBER: 09/240,639
PRIOR FILING DATE: 1999-01-29
NUMBER: OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                                                    380
                                                                                                271 FLAMLLQNSPTKNHLTNPCYPRDYSISFTWGHVFDSLCTVDQRPESYNPNDVITFEGTGD 330
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34.9%; Score 942.5; DB 4
39.8%; Pred. No. 1.1e-90;
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CURRENT PELLING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 6049
 2001-08-06
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39.8%;
CURRENT FILING DATE: 2001-0
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                            Best Local Similarity 39.8 Matches 191; Conservative
                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-949-016-6049
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                                                                     LENGTH: 529
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ORGANISM:
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APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna Maria
FILE REPERBORG: 28110/36120B
CURRENT APPLICATION NUMBER: US/09/905,732B
CURRENT APPLICATION NUMBER: US/09/240,639
PRIOR APPLICATION NUMBER: 09/240,639
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 32
SOFFWARE: PatentIn version 3.1
SEQ ID NO 4
   441 GKIQGSDAGWTIGYMLNLTNMIPAEQPL-STPLSHSTYVFLMVLFSLVLFTVAIIGLLIF 499
                     85 RVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEEL 144
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APPLICANT: JIANG, FENG
TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
FILE REPERENCE: UTSC: 6580S
CURRENT APPLICATION NUMBER: US/09/923,304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 942.5; DB 4; Length
; Pred. No. 1.1e-90;
90; Mismatches 186; Indels
                                                                                                                        ; Sequence 4, Application US/09905732B
; Patent No. 6787328
; GENERAL INFORMATION:
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39.8%;
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Best Local Similarity 39.8'
Matches 191; Conservative
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US-09-905-732B-4
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US-09-923-304-4
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Sequence 6049, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
                                                                                                                                                                                                                                   85 RVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHOETPVYLGATAGMRLLRMESEEL 144
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93 SVKGSGISSYGNNPQDVPRAFEECMQKVKGQVPSHLHGSTPIHLGATAGMRLLRLQNETA 152
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Length 529;
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DB 4;
                                                        90; Mismatches 186;
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Pred. No. 1.1e-90;
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Sequence 11328, Application US/09949016
Facent No. 681239
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 05/241,755
FILE REPERIOR OF TELLOR DATE: 2000-04-14
FRIOR FILING DATE: 2000-10-20
FRIOR PELLOATION NUMBER: 60/241,755
FRIOR PLILING DATE: 2000-10-03
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR PLILING DATE: 2000-09-08
FRIOR PLILING DATE: 2000-09-08
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FRIOR PLILING
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     205 NQETFGALDLGGASTQVTFVPQNQTIESPDNALQFRLYGKDYNVYTHSFLCYGKDQALWQ 264
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39.6%; Pred. No. 3.2e-90;
iive 90; Mismatches 187;
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Best Local Similarity 39.64
Matches 190; Conservative
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APPLICANT: Chadwick, Brian Paul
APPLICANT: Crischauf, Anna Maria
APPLICANT: Frischauf, Anna Maria
APPLICANT: Frischauf, Anna Maria
TITLE OF INVENTION: ACIDS
TITLE OF INVENTION: ACIDS
FILE REFERENCE: 28110/36120C
CURRENT APPLICATION NUMBER: 09/240,639
FRIOR APPLICATION NUMBER: 09/240,639
FRIOR APPLICATION NUMBER: 09/240,639
FRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
     7;
                                                                                                                                                                         93 SVKGSGISSYGNNPQDVPRAFEECMQKVKGQVPSHLHGSTPIHLGATAGMRLLRLQNETA 152
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       Gaps
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39.8%; Pred. No. 1.1e-90;
tive 90; Mismatches 186;
  Mismatches 186;
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90;
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34.9%
Best Local Similarity 39.8%
Matches 191; Conservative
Conservative
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; ORGANISM: Homo Sapiens
US-09-905-743B-4
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US-09-905-743B-4
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Search completed: September 21, 2005, 16:22:30 Job time : 30 Becs

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PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: PCT/US99/22955
PRIOR APPLICATION NUMBER: PCT/US99/22955
NUMBER OF SEQ ID NOS: 31
SGQ ID NO 2
LENGTH: 510
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Deerrintion		Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	0	Sequence 2, Appli	Seguence 297, App	Sequence 97, Appl	Sequence 38, Appl	Sequence 27, Appl	Sequence 2, Appli	Sequence 6, Appli
r.		US-09-835-147-2	US-09-374-586-1	US-09-781-796B-1	US-10-646-308-30	US-10-922-378-2	US-10-934-998-297	US-10-934-998-97	US-10-092-063-38	US-09-835-147-27	US-09-374-586-2	US-09-835-147-6
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Query Match 100.0%; Score 2698; DB 9; Length 510; Best Local Similarity 100.0%; Pred. No. 1.3e-233; Matches 510; Conservative 0; Mismatches 0; Indels 0;

TYPE: PRT ORGANISM: Homo sapiens US-09-835-147-2

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GENERAL INFORMATION

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APPLICANT: SVIGNY, Jean

APPLICANT: BACH, Fritz H.

APPLICANT: BACH, Fritz H.

APPLICANT: ROBSON, Simon

TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT

TITLE OF INVENTION: TECHNOLOGY

TITLE OF INVENTION: TECHNOLOGY

TITLE OF INVENTION: TECHNOLOGY

TITLE OF INVENTION: TECHNOLOGY

TITLE OF INVENTION: TECHNOLOGY

TITLE OF INVENTION: TECHNOLOGY

TITLE OF INVENTION: TECHNOLOGY

TITLE OF INVENTION WIMBER: US/09/781,796B

CURRENT FILING DATE: 1995-04-10

PRIOR FILING DATE: 1995-04-10

PRIOR FILING DATE: 1996-04-10

PRIOR FILING DATE: 1998-02-01

WUMBER OF SEQ ID NOS: 8

SOFTWARE: PATCHTIN VET: 2.1

SEQ ID NO
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181 TINYLLGKFSQKTRWFSIVPYETNNQETFGALDLGGASTQVTFVPQNQTIESPDNALQFR 240
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100.0%; Score 2698; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.3e-233;
Matches 510; Conservative 0; Mismatches 0;
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  TINYLLGKFSOKTRWFSIVPYETINVQETFGALDLGGASTQVTFVPQNQTIESPDNALQFR
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Patent No. US20020138858A1
BERREAL INFORMATION:
APPLICANT: PINSKy.
TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND TITLE OF INVENTION: ISCHEMIC DISORDERS
TITLE REFERENCE: 0575/59167
CURRENT APPLICATION NUMBER: US/09/374,586
CURRENT PILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
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100.0%; Score 2698; DB 9; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.3e-233;
Matches 510; Conservative 0; Mismatches 0; Indels 0
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TYPE: PRT
ORGANISM: HOMO-SAPIEN
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WS-10-922-378-2

Sequence 2, Application US/10922378

Publ.deation No. US20050169968A1

GENERAL INFORMATION:
APPLICANT: ELMALEH, DAVID R.
APPLICANT: RELMALEH, DAVID R.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION WINDER: US/10/922,378

CURRENT APPLICATION NUMBER: US/10/922,378

CURRENT APPLICATION NUMBER: GO/4.01

CURRENT APPLICATION NUMBER: 60/358,303

PRIOR APPLICATION NUMBER: 60/358,303

PRIOR FILING DATE: 2002-02-19

PRIOR FILING DATE: 2002-02-20

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PATENTIN Ver. 3.3

SOFTWARE: PATENTIN Ver. 3.3
                                      SLLLQGYHFTADSWEHIHFIGKIQGSDAGWTLGYMLNLTNMIPAEQPLSTPLSHSTYVFL 480
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100.0%; Score 2698; DB 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-233;
Matches 510; Conservative 0; Mismatches 0;
                                                                                                                          MVLFSLVLFTVAIIGLLIFHKPSYFWKDMV 510
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US-10-922-378-2
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CTKR FEMTL PFQQFEIQGIGNYQQCHQSILELFNTSYCPYSQCAFNGIFL PPLQGDFGAF
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 30. Application US/10646308

Publication No. US20040136992A1

GENERAL INFORMATION:
APPLICANT: BURTON, Paul B. J.
APPLICANT: DEISHER, Theresa A.
TITLE OF INVENTION:
CURRENT APPLICATION COMPOSITIONS AND METHODS FOR FILE REFERENCE: 3432-B

CURRENT APPLICATION NUMBER: US/10/646,308

CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: --to be assigned---
PRIOR APPLICATION NUMBER: 60/406,418

PRIOR FILING DATE: 2003-08-12

PRIOR FILING DATE: 2003-08-12

PRIOR FILING DATE: 2003-08-12

SOFTWARE: PATENTION NUMBER: 61/406,418

CUMBER OF SEQ ID NOS: 36

SOFTWARE: PATENTIN NOWER: SEQ ID NO 30

LENGTH: 510

TYPE: BRT

CRABAISM: Homo sapiens
US-10-646-308-30
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Sequence 97, Application US/10934998
Publication No. US20050153917A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-092-063-38
                                  US-10-934-998-97
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                                                                            Sequence 297, Application US/10934998

Sequence 297, Application No. US20050153917A1

GENERAL INFORMATION:
APPLICANT: AL-MAHMOOD, SALWAN
APPLICANT: COLIN, SYLVIE
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATION THEREOF
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATION WHBER: US/10/934,998
CURRENT FILING DATE: 2004-09-03
PRIOR PAPLICATION NUMBER: PRO2/02717
PRIOR APPLICATION NUMBER: FRO2/02717
PRIOR PELING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 301
SOFTWARE: Patentin version 3.2
SEQ ID NO 297
LENTH: 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: CDS protein of the sequence Genbank/S73813 (seq ID 290)
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100.0%; Pred. No. 1.3e-233;
tive 0; Mismatches 0;
MVLFSLVLFTVAIIGLLIFHKPSYFWKDMV 510
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Best Local Similarity 100.
Matches 510; Conservative
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APPLICANT: AL-MAHWOOD, SALMAN
APPLICANT: AL-MAHWOOD, SALMAN
APPLICANT: COLIN, SYLVIE
APPLICANT: COLIN, SYLVIE
APPLICANT: COLIN, SYLVIE
APPLICANT: COLIN, SYLVIE
APPLICANT: CHESTOPHE
TITLE OF INVENTION: GENERALIONS CONTAINING SAME AND APPLICATIONS THEREOF
FILE REFERENCE: BAN-04-1206
CURRENT APPLICATION NUMBER: US/10/934, 998
CURRENT PILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: FR02/02717
PRIOR APPLICATION NUMBER: FR02/02717
PRIOR FILING DATE: 2002-03-04
PRIOR FILING DATE: 2002-03-04
PRIOR PLILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 301
SSOFTWARE: Patentin version 3.2
LENGTH: 517
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CRVKGPGISKFVQKVNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEE 143
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                                                                                           GENERAL INFORMATION:
APPLICANT: Maliazewski, Charles R.
APPLICANT: Maliazewski, Charles R.
APPLICANT: Brice, Virginia L.
APPLICANT: Gampel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE OF INVENTION NUMBER: US 60/104,585
PRIOR PELICATION NUMBER: US 60/107,466
PRIOR PELING DATE: 1999-10-16
PRIOR PELING DATE: 1999-10-16
PRIOR PLING DATE: 1999-10-13
PRIOR PLING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 27
LENGTH: 464
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER TAP-SPAATION: construct of human CD39
US-09-835-147-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 87.4%; Score 2358; DB 9; Best Local Similarity 97.8%; Pred. No. 4.5e-203; Matches 443; Conservative 2; Mismatches 8;
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Patent No. US20020002277A1
GENERAL INFORMATION:
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US-09-374-586-2
, Sequence 2, Application US/09374586
, Parent No. US20020138858A1
, GENERAL INFORMATION:
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                                                                                              APPLICANT: FOLG.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
FILE REFERENCE: 28110/35908
CURRENT APPLICATION NUMBER: US/10/092,063
CURRENT FILING DATE: 2002-03-05
PRIOR PILLING DATE: 2002-01-05
PRIOR FILING DATE: 1999-07-16
PRIOR PLILING DATE: 1999-07-16
PRIOR PLILING DATE: 1999-07-16
PRIOR PLILING DATE: 1999-07-09
PRIOR PLILING DATE: 1999-07-09
PRIOR PLILING DATE: 1999-07-09
PRIOR PLILING DATE: 1999-03-09
PRIOR FILING DATE: 1999-07-04
PRIOR FILING DATE: 1999-07-04
PRIOR FILING DATE: 1999-07-04
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PRIOR FILING DATE: 1999-07-06
PRIOR FILING DATE: 1999-07-06
PRIOR FILING DATE: 1999-07-06
PRIOR FILING DATE: 1999-07-06
PRIOR FILING DATE: 1999-07-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-092-063-38
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LENGTH: 502
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APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Frice, Vicquia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
PRIOR FILING DATE: 1998-10-16
PRIOR PELICATION NUMBER: US 60/104,585
PRIOR PELICATION NUMBER: US 60/107,466
PRIOR PILING DATE: 1998-11-06
PRIOR PILING DATE: 1998-10-16
PRIOR PILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                  1 TONKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVECRVKGPGISKFVQK
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APPLICANT: Pinsky, David J.

TITLE OF INVENTION: CD39/ECTO-ADPASE AS A TREATMENT FOR THROMBOTIC AND TITLE OF INVENTION: 1SCHEMIC DISORDERS
FILE REFERENCE: 0575/59167
CURRENT APPLICATION NUMBER: US/09/374,586
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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100.0%; Pred. No. 3.3e-202;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 439; Conservative
                                                                                                                                                         ; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-374-586-2
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Sequence 30, Application US/09835147

Sequence 30, Application US/09835147

Sextent No. US2002002277a1

GENERAL INFORMATION:

APPLICANT: Maliszewski, Charles R.

APPLICANT: Maliszewski, Charles R.

APPLICANT: Gimpel, Steven D.

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2979-US

CURRENT APPLICATION NUMBER: US/09/835,147

CURRENT APPLICATION NUMBER: US 60/104,585

PRIOR REPLICATION NUMBER: US 60/104,666

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1999-10-13

PRIOR PLILOGATION NUMBER: US 60/149,010

PRIOR PLILOGATION NUMBER: PCT/US99/22955

PRIOR PELICATION NUMBER: PCT/US99/22955

PRIOR PELICATION NUMBER: PCT/US99/22955

PRIOR FILING DATE: 1999-10-13

NUMBER OF FILING DATE: 1999-10-13

NUMBER OF FILING DATE: 1999-10-13

SEQUENCE: BASED ID NOS: 31

SEQUENCE: BASED ID NOS: 31

TYPE: PRI
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                                                                                                                                                                         Description of Artificial Sequence: Fusion construct of human CD39
                                                                                                                                                                                                                                                                                                 454;
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                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description
OTHER INFORMATION: construct
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 454
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VNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLLRMESEELADRVLDVVERSLS 157
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APPLICANT: Gayle III, Richard B.
APPLICANT: Gayle III, Richard B.
APPLICANT: Frice, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REPERENCE: 2979-US
CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 2001-04-13
PRIOR FILING DATE: 1998-10-16
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1998-11-06
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
NUMBER: OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                      35 TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQK
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                                                                                                                              38 TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQK
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                                                                                    0; Indels
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                                         87.0%; Score 2348; DB 9; I
100.0%; Pred. No. 3.7e-202;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 28, Application US/09835147; Patent No. US20020002277A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 439; Conservative
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Best Local Similarity
      US-09-835-147-29
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LENGTH: 474
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Patent No. US2002000227741

GENERAL INFORMATION:

APPLICANT: Maliszewski, Charles R.

APPLICANT: Maliszewski, Charles R.

APPLICANT: Gimpel, Stewen D.

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2879-US

CURRENT APPLICANTION: UNMER: US/09/835,147

CURRENT PILING DATE: 1998-10-16

PRIOR PILING DATE: 1998-10-16

PRIOR PLING DATE: 1998-11-06

PRIOR PLING DATE: 1999-10-13

PRIOR PLING DATE: 1999-10-13

PRIOR PLING DATE: 1999-10-13

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 29

LENGTH: 473
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion
OTHER INFORMATION: construct of human CD39
                                             Fusion
                                                                                                                              Length 463
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                                         OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: construct of human CD39
                                                                                                                         Query Match

87.0%; Score 2348; DB 9; L
Best Local Similarity 100.0%; Pred. No. 3.5e-202;
Matches 439; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence FEATURE:
                                                                 ; OTHER INFORM;
US-09-835-147-30
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Sequence 3, Application US/09835147

Sequence 3, Application US/09835147

GENERAL INFORMATION:

APPLICANT: Maliszewski, Charles R.

APPLICANT: Gimpel, Steven B.

APPLICANT: Gimpel, Steven D.

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2879-US

CURRENT APPLICATION NUMBER: US/09/835,147

CURRENT APPLICATION NUMBER: US 60/104,585

PRIOR PILING DATE: 1998-110-16

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-10-13

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-10-13

SPIOR PILING DATE: 1999-10-13

SEQUID NOS: 31

SEQUID NOS: 31

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SEQUID NOS: 31
                                           TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 87.0%; Score 2348; DB 9; L Best Local Similarity 100.0%; Pred. No. 3.7e-202; Matches 439; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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38 TQNKALPENVKYGIVLDAGSSHTSLYIYKWPAEKENDTGVVHQVEECRVKGPGISKFVQK 97
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                                                                       VNEIGIYLTDCMERAREVIPRSQHQETPVYLGATAGMRLIRMESEELADRVLDVVERSLS
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Sequence:

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AP037366 Mus muscu
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AF05940 Bos tauru
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AJ13134 Homo sapi
AX828501 Sequence
BC073267 Xenopus 1
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: C12N15/09, A61K38/00, A61P9/00, C07K14/705, C12N1/15, C12N1/19, PC
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Inhibitors of platelet activation and recruitment.
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/organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
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100.0%; Score 1365; Best Local Similarity 100.0%; Pred. No. 0; Matches 1365; Conservative 0; Mismatches
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BD226698 Inhibitor
U87967 Human ATP d
AR168353 Sequence
AX82664 Sequence
AX82664 Sequence
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AX82400 Sequence
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Copyright (c) 1993 - 2005 Compugen Ltd.
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PD 27-A02-2002
PN 3-A0CT-1999 JP 2000577185
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PI CHARLES R MALISZEWSKI,RICHARD B GAYLE III,VIRGINIA L PRICE, PI STEVBN D GIMPEL
PC C12N15/09,A61K38/00,A61P9/00,C07K14/705,C12N1/15,C12N1/19, PC
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1 (bases 1 to 1464)
Maliazewski,C.R., Iii,R.B.G., Price,V.L. and Gimpe,S.D.
Inhibitors of platelet activation and recruitment
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PN 201215/09, AG1K38/00, AG1P9/00, CO7K14/705, C12N1/15, C12N1/19, F
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PC C12P21/02//C12N9/14,C12N15/00,A61K37/02,C12N5/00
Inhibitors of platelet activation and recruitment FH
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Location/Qualifiers

    1599
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    /db_xref="taxon:9606"

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Best Local Similarity 99.8%;
Matches 1321; Conservative
                          Homo sapiens (human)
Homo sapiens
 BD228698.1 GI:330
JP 2002527096-A/1
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TYLTOCMERARBVI RRSQHQBTPVYLGATAGMRLLRMBSEBLADRYLDVVBRSLSNY
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                                                                                                                                                                                      3 (bases 1 to 1704)
Kaczmarek, E., Koziak, K., Sevigny, J., Siegel, J.B., Anrather, J.,
Beaudoin, A.R., Bach, F.H. and Robson, S.C.
Direct Submission
Submitted (30-JAN-1997) Medicine, Harvard University, 99 Brookline
Avenue, BIDMC, RN, Boston, MA 02215, USA
Location/Qualifiers
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                                                        Robson, S.C., Kaczmarek, E., Siegel, J.B., Candinae, D., Koziak, K. Millan, M., Hancock, W.W. and Bach, F.H.
Lose of ATP diphosphohydrolase activity with endothelial cell activation
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I (basea I to 1704)
Kaczmarek, E., Koziak, K., Sevigny, J., Siegel, J.B., Anrather, J., Beaudoin, A.R., Bach, F.H. and Robson, S.C.
ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAAGGACATTCAGGTTGCAAGTAATG
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Beaudoin, A.R. and Sevigny, J.
Mammalian ATP-diphosphohydrolases and process of purification
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Pred. No. 0;
0; Mismatches
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Patent: US 6287837-A 2 11-SEP-2001;
Location/Qualifiers
1. .1818
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/mol_type="unassigned DNA"
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ल में ल में		JOURNAL Patent: WO 03074073-A 290 12-SEP-2003;  JOURNAL Patent: WO 03074073-A 290 12-SEP-2003;  Gene Signal (FR)  Gene Signal (FR)  Cocation/Qualifiers  11818  /mol_type="unassigned DNA"  /db_xref="taxon:9606"  Onerv Match  96.6%: Score 1319.2; DB 6: Length 1818:	Best Local Similarity 99.8%; Pred. No. 0;  Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps  41 GTTCAACCCAGAACAAAGCATTGCCAGAAACGTTAAGTATGCGATTGTGTGCAGATGCGG  174 GGTTGACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGCGATTGTGCTGGATGCGG  101 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGCGAGAATGCGAAGAATGCGAAGAATGCGAAGAATGCGAAGAATGCGAAGAAAGGAAAAGGAAAAGGAAAAGAAGAAGAAGAAG	Db 234 GTTCTTCTCACACAGTTTATACATCTTTATAGGCCAGCAGAAAGGAGAATGACACAG 293  Qy 161 GCGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTGTTC 220  Db 294 GCGTGGTGCATCAAGTAGAAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC 353  Qy 221 AGAAAGTAAATGAAATAGGCATTTACCTGATTGCATGAAAGAGTCAGGGAAGTGA 280  Db 354 AGAAAGTAAATGAATTAGCTGATTGATTGCATGAAAGAGCTAGGGAAGTGA 413  Qy 281 TTCCAAGGTCCAGCACCAAGAACACCCGTTTACCTGGGAAGCCAGGCATGGGAATGGAA 413  Db 414 TTCCAAGGTCCCAGCACCAACAAGAACACCTGAGGAACCACGGCAGGCA	QY         341 TGCTCAGGATGGAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGAGAGGAGCC 400           Db         474 TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGCC 533           QY         401 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATACTGGCCAAGAGGAAGTG 460           Db         534 TCAGCAACTACCCCTTTGACTTCCAGGTGCCAGGATCATACTGGCCAAGAGGAAGTG 593           QY         461 CCTATGGCTGGATTACTATCAACTATCTGCTGGGCAAATTCAGTCAG

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    GAGCCTCTACACACACACTTTTCTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG
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Poindexter, K., Birke, C. et, al.

The CD39 lymphoid cell activation antigen. Molecular cloning and structural characterization
J. Immunol. 153 (8), 3574-3583 (1994)
95015846
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GenBank Staff at the National Library of Medicine created this entry [NCBI gibbeq 156681] from the oxiginal journal article.
Location/Qualifiers
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/note="lymphoid cell activation antigen,
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                                                                                                                                                                                                                                                                        /gene="CD39"
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diphosphatase homolog"
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Homo sapiens mRNA for ecto-ATP diphosphohydrolase, isolate C1800. AJ131133 AJ131133 GI:4741544 ecto-ATP diphosphohydrolase, isolate C1800. Homo sapiens (human) sapiens sapiens sapiens
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                             GTTACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTTCTTGCCACCACTCCAGGGG 1000
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Titani,K., Fujimura,Y. and Narita,N.
The cDNA cloning of human placental ecto-ATP diphosphohydrolases I
and II
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (23-FEB-1999) Matsumoto M., Department of Blood
Transfusion Medicine, Nara Medical University, Kashihara,
Nara, 634-8522, ARPN
Location/Qualifiers
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/db_xref="taxon:9606"
/tisue_type="placenta"
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184. 1737
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Genes involved in regulating angiogenesis, pharmaceutical preparations containing same and applications thereof Patent: WO 03074073-A 46 12-SEP-2003; Gene Signal (FR)
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/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Novel therapeutic targets in cancer
Patent: WO 2004074320-A 693 02-8EP-2004;
Sagres Discovery, Inc. (US)
Location/Qualifiers
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Morris,D.W., Morris,D.W. and Malandro,M.S
Novel therapeutic targets in cancer
Patent: WO 2004074320-A 691 02-SEP-2004;
Sagres Discovery, Inc. (US)
Location/Qualifiers
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99.8%; Pred. No. 0;
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Oy 1301 TGAACCTGACCAACATCCAGGTGAGCAACCATTGTCCACCTCCACTCCA 1360

Db 1444 TGAACCTGACCAACATGATCCCAGCTGAGCAACCATTGTCCACCTCTCCCACTCCA 1360

Qy 1361 CCTA 1364

Db 1504 CCTA 1507

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Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombus formation; occlusion; restenosis; anglogenesis; antianginal; cerebroprotective; antitorodus disported; cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; ds.
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/note= N-terminus of mature human interleukin 2 (IL2)"
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/note= "Coding region of human soluble CD39 (solCD39)"
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AACTATCTGCTGGGCAAATTCAGTCAGAAAACAAGGTGGTTCAGCATAGTCCCATATGAA
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The present cDNA sequence is a fusion construct encoding sol(soluble) CD19 having apyrase activity. Fusion of 12 amino acids from the N-terminus of mature human L12 to the solCD39 coding region results in high levels of both expression and activity in the supernatants of transfected cells. This is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic sischaemia, a thrombosia, embolism, platelet-associated ischaemic ischaemia, a thrombosis, including occonary attery thrombosis, cerebral attery thrombosis, including coronary artery thrombosis, thrombosis, coagulopathy, deep venous thrombosis (bT), pulmonary embolism (PE), transfent ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or restenosis of blood
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cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; peripheral artery thrombosis; cosquiopathy; deep venous thrombosis; DVT; PE; pulmonary emboliam; transient ischaemic attack; thrombus formation; occlusion; reocclusion; stenosis; restenosis; antianginal; cardiant; cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant; coronary ischaemia; vascular occlusion; ss.
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mature N-terminus of hIL2 and soluble CD39 (solCD39) coding region, having apyrase activity. This produces high levels of solCD39 expression and activity in the transfected cells. Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and cereminat, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting angiogenesis. It is useful for the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, precelampsia, cor injury, atherosclerosis, peripheral vascular occlusion, precelampsia, coronary and cerebral ischaemia, thrombosis, disorders including lung, coronary and cerebral ischaemia, thrombosis, disorders including coronary, thrombosis, coagulopathy, deep venous thrombosis (DTF), pulmonary embolism (PE) and transfent ischaemic attack. Soluble CD39 is also useful cor preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke
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                              ATCCAGGGCAGCGAGCTGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACAACATGATC 1320
                                                                                                                                                                                                                                                                                                                                 Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombos formation; occlusion; restenosis; anglogenesis; antianginal; cerebroprotective; antiarteriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present DNA sequence is a fusion construct pIL2LsolCD39, comprising leader peptide of human interleukin 2 (hIL2), 12 amino acids from the
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/note= "Coding region of human soluble CD39 (solCD39)"
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                                                                              CCAGCTGAGCAACCATTGTCCACACCTCTCTCCCACCTCAA 1365
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        TGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATGAAATTCTCAGGGACCCATGC
                           TITCATCCTGGATATAAGAAGGTAGTGAACGTAAGTGACCTTTACAAGACCCCCTGCACC
                                                                                                                     CTTCTGCAAGGCTATCATTCACAGCTGATTCCTGGGAGCACCACTCCATTTCATTGGCAAG
                                       TTTCATCCTGGATATAAGAAGTAGTGAACGTAAGTGACCTTTACAAGACCCCCTGCACC
                                                                  AAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAATCCAGGGTATTGGAAACTAT
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The present sequence is coding region of pIL2SolCD39, a fusion construct encoding sol (soluble) CD39 having apyrase activity. Fusion of 12 amino acids from the N-terminus of mature human IL2 to the solCD39 coding region results in high levels of both expression and activity in the supernatants of transfected cells. This is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder including lung including coronary ischaemia and cerebral ischaemia, thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis, ransient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke
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                                                                                "Mature human IL2 protein"
note= "human IL2 leader sequence"
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Matches 1365; Conservative
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Soluble CD39; solCD39; human; apyrase activity; platelet activation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; pulmonary embolism; PE; thrombos formation; occlusion; restenosis; angiogenesis; antianginal; cerebroprotective; antiateriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; ds.
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/note= "Coding region of human soluble CD39 (solCD39)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Mature human interleukin 2 N-terminal end"
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product= "Fusion protein of pIL2LFlagSolCD39"
              1365
                              1393 CCAGCTGAGCAACCATTGTCCACACCTCTCTCCCACTCCACCTAA 1437
                                                                                                                                                                                                                  Human soluble CD39 fusion DNA construct, pIL2LFlagSolCD39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "Human interleukin 2 (hIL2) leader
              CCAGCTGAGCAACCATTGTCCACACCTCTCTCCCACTCCACCTAA
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acids from the mature N-terminus of hill, a linker, FlAG tag sequence and soluble CD39 (solCD39) coding region, that has apyrase activity. This produces high levels of solLD39 expression and activity in the transmemelation of sollops expression and activity in the transmembrane domains. It retains the capacity to metabolise ATP cerminal transmembrane domains. It retains the capacity to metabolise ATP concentrations and the ability to block and reverse ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting considerable and recruitment, including platelet aggregation. Struke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, creatment of instable angina, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, creatment ischaemia, thrombosis, including lung, coronary and cerebral artery thrombosis, intracardiac and venous thrombosis, and cerebral artery thrombosis, lung, pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, reocclusion, stenosis or restenosis or stroke
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                                                                                                                                            GATATAAGAAGGTAGTGAACGTAAGTGACCTTTACAAGACCCCCTGCACCAAGAGATTTG
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                                                                                                               GATATAAGAAGGTAGTGAACGTAAGTGACCTTTACAAGACCCCCTGCACCAAGAGATTTG
                                                                                                                                                                                                                                                                              950 AGATGACTCTTCCATTCCAGCAGTTTGAAATCCAGGGTATTGGAAACTATCAACAATGCC
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                            290 TTAAAGGTCCTGGAATCTCAAAATTTGTTCAGAAAGTAAATGAAATGAAATGGCATTTACCTGA
                                                                    CTGATTGCATGGAAAGAGCTAGGGAAGTGATTCCAAGGTCCCAGCACCAAGAGACACCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the coding region of soluble CD39(solCD39) protein in mammalian expression systems. SolCD39 is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, precelampsia, embolism, platelet-associated ischaemic disorder including ischaemia, coronary ischaemia and cerebral ischaemia, a thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, thrombosis, thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DYT), pulmonary embolism (PB), transfent ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke
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/note= "First N-terminal 12 amino acids"
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(CORR ) CORNELL RES FOUND INC
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Best Local Similarity 98.5%;
Matches 1334; Conservative
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embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, stenosis or restenosis of blood vessels or stroke
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                                    1429
                                                                                                                                                                                                                                                                                                                           Soluble CD39; human, apyrase activity; platelet activation; inhibitor; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preclampsia; embolism; platelet-associated ischaemic disorder; thrombotic disorder; reocclusion; coagulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE; thrombos formation; occlusion; stenosis; restenosis; angiogenesis; antianginal; cerebroprotective; antiateriosclerotic; anticoagulant; cardiant; vasotropic; thrombolytic; ss.
1370 GCGACCCCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATCCCAGCTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New soluble CD39 polypeptides having apyrase activity, useful for inhibiting angiogenesis and treating unstable angina, myocardial infarction, stroke, coronary artery disease or injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human soluble CD39 protein"
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                                                                                                    GTACCTACATTCTCTCCCTCCTTCTGCAAGGCTATCATTTCACAGGCTGATTCCTGGGAGC
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                                                                     <u>aagretereaggaaaaggreacreagargargaaaaaagtrergreereageerregeaag</u>
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                                                                                          AGATAAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTG
                                                                                                                                                                                                                              1433 TGAACCTGACCAACATGCTCCAGCTGAGCAACCATTGTCCACACTCTCTCCCCACTCCCA
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/product= "Soluble CD39
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The present cDNA sequence encodes soluble CD39 having apyrase activity.

This was derived from a cDNA library prepared from a human B cell line

creferred to as MP-1. Soluble CD39 retains the capacity of wildtype CD39

Cr metabolise ATP and ADP at physiologically relevant concentrations as

concentrations as the ability to block and reverse ADP-induced platelet activation

and recruitment including platelet aggregation. This is used in the

creatment of unstable angina, myocardial infarction, stroke, coronary

cartery disease or injury, atherosclerosis, peripheral vascular occlusion,

creclampsia, embolism, platelet-associated ischaemia disconder including

coronary ischaemia, and exceptal ischaemia, a thrombocic

disporder including coronary artery thrombosis, cerebral artery

chrombosis, intracardiac thrombosis, peripheral artery thrombosis, thrombosis, coagulopathy, deep venous thrombosis, venous

thrombosis, thrombosis, coagulopathy, deep venous thrombosis, (DVT),

chimonary embolism (PE), transient ischaemic attack Soluble CD39 is also

cuseful for preventing thrombus formation or reformation, occlusion,

crecclusion, stenosis or restenosis of blood vessels or stroke
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Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39
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                                                                                                                                                                                                                                          Example 10; Page 85-87; 118pp; English.
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                                                                                                                                                                                                                                                                                            The present invention relates to a method of treating cardiovascular disease in a subject, comprising administering an IL-17, IL-18, 4-1BB CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists are useful for treating cardiovascular disorders, e.g. (chronic immune) myocarditis, congestive heart failure, aneurysms, angina, embolism, restanosis, ischaemia or thrombocytopenic purpura, present sequence is a coding sequence used in the exemplification of invention.
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                                                                                                                                                                                                          Use of IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists, for treating a cardiovascular disease, e.g. chronic immune myocarditis, congestive failure, aneuryem, angina, embolism, restenosis, ischemia or thrombocytopenic purpura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1599;
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                       Disclosure; Page 130-132; 135pp; English
                                                                                   28-AUG-2002; 2002US-0406418P.
12-AUG-2003; 2003US-0494457P.
                                                                                                                                                                                                                                                                                                                                                                                                                                  96.6%;
                                                            21-AUG-2003; 2003WO-US026354
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            WO2004019866-A2
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Matches 1321;
                                   11-MAR-2004
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                                                                     ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATG
                                                                                                                                                        TTTACAAGACCCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAA
                                                                                                         AAATTCTCAGGGACCCATGCTTTCATCCTGGATATAAGAAGGTAGTGAACGTAAGTGACC
                                                                                                                                                                                                         TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Increasing or decreasing drug resistance in target bacteria, yeast, plant or mammalian cells comprises altering ATP gradient across biological membrane of target cell.
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                                                                                                                                                                                                                                                                                          The present invention relates to a method for increasing or decreasing drug resistance in target bacteria, yeast, plant or mammalian cells by altering the ATP gradient across the biological membrane of the target cell. The method is useful for modulating drug resistance of cells. It inseful for increasing the sensitivity of cells to chemotheraputic and antibiotic agents and increasing resistance to herbicides. The present sequence is human ATP diphosphohydrolase coding sequence. This sequence encodes was used in the present invention to modulate drug resistance. Note: The present sequence is not shown in the specification, but is referred to via its GenBank accession number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GITCITCICACACACAGITIATACAICTATAAGIGGCCAGCAGAAAAGGAGAAIGACACAG
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96.6%; Score 1319.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches
                                                                                                                                                       Lloyd
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                                                                                                                                                                                                                                                                      Claim 14; Page; 85pp; English.
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                                                                                                                           (TEXA ) UNIV TEXAS
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The invention relates to a conjugate (1) comprising an enzyme and a biodegradable polymer, where (i) enzymatic activity of the enzyme is conjugate to this that of the enzyme in the absence of the blodegradable polymer. Treature to that of the enzyme is longer than that of the conjumer, or (ii) the half life of the enzyme is longer than that of the enzyme in the absence of the polymer. The enzymetic activity (1) is at carryme in the absence of the polymer. The enzyme is a multimeric, soluble and/or extracellular enzyme, preferably an apyrase, especially a soluble form of CD39 and catalyzes or preferably an apyrase, especially a soluble form of CD39 and catalyzes or preferably an apyrase, particularly cardiovascular disease. Concer, sepais or adjensed diphosphate. The conjugate can be used to treat chrommal aggregation of platelets, particularly cardiovascular disease, concer, sepais or adjense related to graft transplant. (I) is also used for treating coronary artery disease or injury following myocardial infarction, unstable angina, atherosclerosis, pre-eclampaia, embolism, careful achaemia, reocclusion following thrombosia, thrombosis, proceediated with exposure to a foreign or injured tissue surface, in combination with angioplasty, carcidovascular devices. The present sequence represents a DNA encoding a human CD39 polypeptide.
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(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
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                                           GAGCCTCTACACAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG
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The bovine aorta (AAW04335 to AAW04318 and AAW04340) and porcine pancreatic (AAW04339) ATPDases have been partially sequenced. The sequences have been found to be highly homologous to a human lymphoid cell activation antigen designated CD39 (Maliszenski et at. (1994). J. Immunol.: 3574-3583). The complete sequences of the ATPDases types I and II have not been obtained yet. Assuming that the CD39 gene product is an ATPDase type II, the use of CD39 in the reduction of platelet aggregation and of thrombogenicity may be contemplated, as well as a process of making ATPDases using the CD39 sequence (AAT38516)
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                                                                                                                                                                                              Human lymphoid cell activation antigen CD39
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/note= "CD39 protein has ATP diphosphohydrolase activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-human transgenic or somatic recombinant mammals, whose cells contain a heterologous DNA encoding a polypeptide (especially human CD39 protein) having ATP-diphosphohydrolase activity under cellular activating conditions is claimed. In particular the animal is a pig and its cells (or tissues or organs) can be used for transplantation. DNA coding for human CD39 is also useful for genetically modifying a mammalian cell to render it less susceptible to an inflammatory or immunological stimulus and platelet aggregation. The modified cells can be used to prevent or alleviate a thrombotic condition. The present sequence encodes human CD39 protein and was disclosed in J.Immunol. 153 (8) (1994) 3574-3584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene therapy of inflammatory or immunological stimulation of platelet aggregation - using CD39 protein with ATP d1:phospho:hydrolase activity, useful for preventing or alleviating thrombotic condition in mammallan
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ATP diphospholydrolase; transgenic animal; pdz; porcine; graft;
transplantation; endothelial cell; prosthetic device;
platelet aggregation; inhibition; intravascular; ds.
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99.8%; Pred. No. 0;
tive 0; Mismatches
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68. .1600
/*tag= a
/EC_number= "3.6.1.5"
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96US-00600383
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11; Conservative
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Human, gene; 88; immunological response; immunopathological condition; Crohn's disease; asthma; ulcerative colitis; Mypereosinophilia; irritable bowel syndrome; osteoarthritis; rheumatoid arthritis; acte monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer; osteopathic; antiarthritic; antirheumatic; cytostatic.

A composition comprising a plurality of CDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma or osteoarthritis.

The invention relates to a composition comprising a plurality of cDNAs for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the treatment of an immunopathological condition is asmple with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes and comparing the levels of the detected hybridisation complexes with the level of hybridisation complexes with the level of hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and contacting a plurality of polynucleotide probes. The CDNAs method for identifying a plurality of polynucleotide probes. The cDNAs are useful as hybridisable array elements in a microarray for monitoring the expression of target polynucleotides. The microarray can be used in

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the diagnosis of an immunopathology, such as Crohn's disease, asthma, ulcerative colitis, hypereosinophilia, irritable bowel syndrome, osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in identifying agents for the treatment of the diseases. The microarray may also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition may also be used in purification of a subpopulation of manAs, cDNAs or genomic fragments. This sequence represents a human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                 GGTTGACCCAGAACATTGCCAGAAAACGTTAAGTATGGGGATTGTGTTGGATGCGG
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                                                                                                                                                                                                                                                    Query Match 96.6%; Score 1319.2; Best Local Similarity 99.8%; Pred. No. 0; Matches 1321; Conservative 0; Mismatches
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The invention relates to a novel pharmaceutical composition active on angiogenesis comprising an endothelial cell nucleic acid whose expression is induced by an angiogenic factor and inhibited by an angiostatic agent or its complement or fragment, a polypeptide sequence encoded by the nucleic acid or its fragment, a molecule capable of inhibiting expression of the nucleic acid or a molecule which binds to the polypeptide sequence. The invention is used to diagnose, prognose or treat an angiogenic disorder in a mammal, particularly a human. The disorder is particularly tumor vascularization, a retinopathy, rheumatoid arthritis, crohn's disease, atherosclerosis, ovary hyperstimulation, psoriasis, endometriosis associated with neovascularization, restenosis due to angioplasty, overproduction of tissue due to cicatrisation, a peripheral vascular disease, hypertension, vascular inflammation, Raynaud disease, aneurism, atterial restenosis, thrombophlebitis, ischemia, angina, mourism acterial restenosis, thrombophlebitis, ischemia, angina, macular degeneration due to age or osteoporosis. This sequence congestion of corresponds to a differentially expressed DNA used in the composition of
   polypeptide differentially expressed in angiogenesis.
                                                        Claim 2; SEQ ID NO 290; 424pp; French
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Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;

580 640 340 520 GGTTGACCCAGAACAATGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGGGG 233 GITCITCICACACAAGIITAIACAICIAIAAGIGGCCAGCAGAAAAGGAGAAIGACACAG 160 293 220 353 280 413 473 400 533 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTG 460 593 653 713 773 833 GTTCTTCTCACACATTATACATCTATAAAGTGGCCAGCAGAAAAGGAGAAATGACACAG GCGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC GCGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGAAGTGA TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGAGGAGGAGGAGCC rcaccaactaccccrrrgacrrccaggcrcccaggarcarracrgcccaagaggaggrg TCAGCATAGTCCCATATGAAACCAATAATCAGGAAAACCTTTGGAGCTTTGGACCTTGGGG CTCTGCAATTTCGCCTCTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCT GTTCAACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGAGGAGGCC cerariegeregarracrarcrarerecresceaarreagreaaaacaagregr Gaps Length 1818; ö 3; Indels DB 12; Score 1319.2; I Pred. No. 0; 0; Mismatches 96.6%; ilarity 99.8%; Conservative Query Match Best Local Similarity Matches 1321; Conserv 174 234 161 414 41 101 294 221 354 281 341 474 401 534 461 594 521 654 581 641 셤 요 ઠે 셤 요 g 8 ò g ò 셤 ઠે 8 g ò g g ò ેં ò

1000 1120 1180 1240 1300 1013 1073 1133 1060 1193 1314 GTACCTACATTCTCTCCTCCTTCTGCAAGGCTATCATTTCACAGGCTGATTCCTGGGAGC 1373 1433 1360 1493 AGATAAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTG 1313 940 760 820 880 893 953 GTTACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCCCACTCCAGGGG AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGG 1374 ACATCCATTTCATTGGCAAGATCCAGGGCAGCGACGCCGGCTGGACTTTGGCTACATGC TGAACCTGACCAACATGATCCCAGCTGAGCAACCATTGTCCACACCTCTCCCCACTCCA 1434 TGAACCTGACCAACATGATCCCAGCTGAGCAACCATTGTCCACACTCTCTCCCCACTCCCA ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATG TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACACCA TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACAC ATTTTGGGGCATTTTCAGCTTTTTACTTTGTGATGAGGTTTTTAAACTTGACATCAGAGA ATTTTGGGGCATTTTCAGCTTTTTACTTTGTGAAGTTTTTAAACTTGACATCAGAGA AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGG AGATAAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTG GTACCTACATTCTCTCCCTCCTTCTGCAAGGCTATCATTTCACAGCTGATTCCTGGGAGC ACATCCATTCATTGGCAAGATCCAGGGCAGCGACGCCGGCTGGACTTTGGGCTACATGC AAATTCTCAGGGACCCATGCTTTCATCCTGGATATAAGAAGGTAGTGAACGTAAGTGACC CCTA 1364 CCTA 1497 1001 1134 1194 1254 1241 1301 894 954 1074 1061 1121 1181 1494 761 821 881 941 1361 셤 à 셤 ò 셤 ò 셤 ઠે g ò ద ò 요 ò q Š 셤 8 g 8 셤 ò

completed: September 21, 2005, 17:05:27 ne : 791.776 secs Search co

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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 910 GENYZ cedex - FRANCE (E-mail : segref@genoscope.cns.fr
191 910 1910 ENYZ cedex - FRANCE (E-mail : segref@genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSFORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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25-normalized
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BP434894
BP434198
AGENCOURT
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Li (W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished
                                                                                                                                                                                      BP170602
BB612808
AL572575
602926181
BP170295
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AU121657
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BP157197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
AL552087
BX402315
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Pred. No. 3.2e-303;
); Mismatches 4;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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CD652289
BP170602
BB612808
ALSS2087
BX402315
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Copyright (c) 1993 - 2005
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                                                                                                                                                                                                                                                                                                    Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 2410)
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    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                      Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-langth to CDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
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Please visit our web site for further details.
URL:http://genome.gec.riken.jp/
URL:http://fancom.gec.riken.jp/
Location/Qualifiers
                                                            cloning
                                        Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921511C05 product:ectonucleoside triphosphate diphosphohydrolase 1, full insert sequence.

AK029512

AK029512.1 GI:26325463
  GCGTGCTGCATCAAGTAGAAGAATGCAGGGTTAAAAGGTCCTGGAATCTCAAAATTTGTTC
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1119 1300 1179 1239 1417 1299 1477 1359 1537

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AK030601

Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330437E10 product:ectonucleoside triphosphate diphosphohydrolase 1, full insert sequence.
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Sciurognathi; Muridae; Murinae; Mus
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AAGACCCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAATCCAG
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                                               AAGGATCAGGCACTCTGGCAGAACTGGCCAAGGACATTCAGGTTGCAAGTAATGAAATT
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High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Mammalia; Eutheria; Rodentia;
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HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                   /note="unnamed protein product; ectonucleoside
triphosphate diphosphobydrolase 1 (MGD|MGT:102805,
GB|NM 009848, evidence: BLASTN, 100%, match=2284)
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                         /tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 863; DB 3; Length 2410;
Pred. No. 1.1e-243;
0; Mismatches 255; Indels 1:
       xref="FANTOM_DB:4921511C05"
xref="taxon:10090"
                                                      /clone="4921511C05"
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79.8%;
                                                                                  /sex="male"
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GB|NM_009848, evidence: BLASTN, 100%, match=2284)
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79.8%; Pred. No. 1.3e-243;
iive 0; Mismatches 255;
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4198
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Batchi, J. Aizawa, K. Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kauka, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakamira, M., Nishi, K., Nomura, K., Numazaki, A., Mista, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sagabo, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                              Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazaama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshikagi,K., Yonada,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
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'clone_Tib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                            the RIKEN Genome Exploration Research Group Phase II Team and the
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://genome.gec.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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/db xref="taxon:10090"
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/strain="C57BL/6J"
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ENVKYGI VLDAGSSHTNLY I YKWPAEKENDTGVVQQLEECQVKGPGI SKYAQKTDEIG
AYLAECMELGTELI PTSKHIQTPVYLCATAGNKLLENGSEGGABVLAAVSTSLKSYP
FDFQGAKI I TGQEGGAYGH TINYLLGRFKLENGSEGGABVLAAVSTSLKSYP
GITFVPQNSTI ESPENSLQPRLYGEDYTYTHSFLCYGKDQALWGKLAKDIQVSGGY
LKDPCFNPGYEKVNAVSELYGTPCTKRFEKKLPFDQFR I QGTGDYECCHQS I LELFNN
KSWEETKTSYPSVKRKYLSBYCFSGAY I LSLLQYNFTDSSWEQIHPMGK I KDSNAGW
TLGYMLANINNI PAEQPLSPPLPHSTYI GLMVLFSLLLVAVAI TGLFIYSKPSYFWKE /proteIn id="BAC27039.1" /db_xref="GI:26326591" /trānslation="MEDIKDSKVKRFCSKNIL1ILGFTSILAVIALIAVGLTQNKPLP 165 225 563 263 GIGCAGCAGITAGAGGAAIGCCAAGIGAAAGGICCIGGAAICICAAAAIAIGCICAGAAA 383 443 345 503 405 465 623 525 683 585 740 645 800 705 860 TCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAGGCGTG TCTCACACCAACCTGTACATCTACAGTGGCCGGCCGAGAAGGAGGAATGACACAGGGGTG 46 ACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGGGTTCT GTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTCAGAAA 444 ACATCCAAGCATCACCAGACTCCTGTCTACCTGGGGAGCCACAGCAGGCATGCGTTGCTT 564 AGCTACCCCTTTGACTTCCAGGGTGCCAAGATCATCACTGGACAAGAGGAAGGTGCCTAT 741 TCCACACAGATCACCTTCGTGCCCCAAAACAGCACTATAGAGTCCCCCAGAAAACTCTCTG AAGGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATGAAATT 226 GTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGATTCCA 384 ACAGATGAAATCGGTGCGTACCTGGCCGAATGCATGGAACTGTCCACCGAACTGATACCA <u> AGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGAGCCTCAGC</u> AACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTGCCTAT 684 CTCATCTCA---GACAGTCAGAAACAGGAAACCTTTGGCGCTTTGGATCTCGGCGGAGCC TCTACACAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATGCTCTG CAATTTCGCCTCTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCTATGGG caarrecercrareeceaegacraracrererezacacacacerrecrereraree 526 ATAGICCCATAIGAAACCAATAAICAGGAAACCITIGGAGCITIGGACCITIGGGGGAGCC 12; Length 4198; Indels

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                                                                                                                         /clone="CSODIO73YD08"
/tissue type="PLACENTA COT 25-NORMALIZED"
/tlone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lat strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                           59.5%; Score 812.4; DB 5; 99.2%; Pred. No. 7.3e-229; ive 0; Mismatches 3;
                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
                                  Location/Qualifiers
                                                         l. .861
/organism="Homo
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BX371889.2 GI:46831287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSDRT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                            AAGACCCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAATCCAG
                                                                                                                                                GGTATTGGAAACTATCAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACACAGTTAC
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-Length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced
Contact: Genoscope
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BX371889/c
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VERSION
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/ DECOLET 16="BAC26037.1"

/ DECOLET 16="BAC26037.1"

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/ Ab_xref="G1:26324566"

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QGYNFTGSSWRQIHFMKXIKOSNAGWTLGYMLNINMIPAEQPLSPPLPHSTYIGLMV

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="skin"
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/dev_stage="10 days neonate"
<1. .1265
  Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Submiro-cho, Taurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                              cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 504 TCAGAAAACAAGGTGGTTCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGG 563
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triphosphate diphosphohydrolase 1 (MGD|MGI:102805,
GB|NM 009848, evidence: BLASTN, 100%, match=2284)
putatīve"
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                                                                                                                                                                                                                                                                                                            prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.5%; Score 743.4; DB 3; 79.2%; Pred. No. 3.4e-208; ive 0; Mismatches 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db xref="FANTOM DB:4732419M16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="4732419M16"
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3563
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Lot 60,770 full-length cDNAs

Lot 60,770 full-length cDNAs

Lot 60,770 full-length cDNAs

S Adachi,J., Aizawa,K., Akimura,T., Hara,A., Hashizume,W.,

Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,

Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,

Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,

Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,

Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,

Katoh,H., Sawai,J., Kohlana,Y., Solana,Y., Murata,M.,

Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,

Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,

Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,

Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,

Murametsu,M., and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                         AK028625

Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732419M16 product:ectonucleoside triphosphate diphosphohydrolase 1, full insert sequence.
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81 ACTCTTCCATTCCAGCAGTTTGAAATCCAGGGTA-TGGAAACTATCAACAAT-CCATCAA 24
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Functional annotation of a full-length mouse cDNA collection
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                         23 AGCATCCT-GAGCTCTTCAACACC
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Mus musculus (house mouse)
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No. 11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Pull-length cDNA libraries and normalization
Intubulished (2001)
On Feb 15, 2001 this sequence version replaced gi:31274964.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Z rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was disested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
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                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0DI073YD08"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

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clone CSODI073YD08 5-PRIME, MRNA sequence.
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AL552123 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA Clone CSODIO59YC11 5-PRIME, mRNA sequence.
AL552123
AL552123.3 GI:45856912
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1 (bases 1 to 897)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31273939.

Contact: Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
                                                                            AGAAAGTAAATGAGAATTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGA
                                                                                                                                                                                            TGCTCAGGATGGAAAGTGAAGAGTTTGGCAGACAGGGTTCTGGATGTGGTGGAGGGGGGCC
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               GCGTGCTTCAACTAGAAGAATCCAGGTTTAAAGGTCCTGGAATCTCAAAATTTGTTC
                                                         AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGA
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GCGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAAGGTCCTGGAATCTCAAAATTTGTTC
                                                                                                                 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTG
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/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site_1: BCORV (destroyed), Site_2: Not!; RNA source pool
of three ovaries, from featles ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."
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Pred. No. 1.6e-203;
0; Mismatches 45; Indels 11; Gaps
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/organism="Homo sapiens"
/mol_types=mxNN"
/db_xref="taxon:9606"
/clone="TMAGE:5724619"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                              BM906668.1 GI:19357047
                                                                                                                              AAATTCTCAGGGACC 775
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825; Conservative
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Contact: Genoscope Control of Sequences of Secondary Contact: Genoscope - Centre National de Sequences of Service Setton Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE Email: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                            BX402316 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI017YB13 5-PRIME, mRNA sequence.
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1. (bases 1 to 1025)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30610946.
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_list strand cDNA was primed with a NotI-oligo(dT)
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
/note="Ist strand cDNA was primes." Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
751 ATGGGAAGGATCAGGCACTCTGGCAGAACTGGCCAAGGACATTCAGGGTGCAAGTAATG
                                                 AAATTCTCAGGGACCCATGCTTTCATCCTGGATATAAGAAGGTAGTGAACGTAAGTGACC
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                                                                          AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGA
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Pred. No. 3.6e-196;
0; Mismatches 3;
                                                                                                                                                851
                                                                                                                                                                             ||::|:||| | || TIWMAARMCCCCGCMCMARARATTTARATGA 897
                                                                                                                                                821 TTTACAAGACCCCTGCACCAAGAGATTTGA
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI017YB13"
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  Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGA 331
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                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db xref="taxon:9606"
/clone="CSODIO59YC11"
/tissue type="FLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_list strand cDNA was primed with a NoII-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODI059AB06QPl&c=5524.f.
Location/Qualifiers
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BX327984 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI073YD08 5-PRIME, mRNA sequence.
BX327984.1 GI:30332721
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digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 952)

(cruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                  GTTCAACCCAGAACAAAGCATTGCCAGAAAACGTTAAAGTATGGGATTGTGCTGGATGCCG
                                                                                                                                                                      GGTTGACCCAGAACAAAGCATTGCCAGAMAACGTTAAGTATGGGATTGTGCTGGATGCGG
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                                                                  Length 1023;
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                                                                Score 697.6; DB 1;
Pred. No. 8.4e-195;
5; Mismatches 5;
                                                                51.1%;
98.6%;
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1. (basea 1 to 1023)

2. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

3. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

4. Unpublished (2001)

5. Ton Feb 15, 2001 this sequence version replaced gi:31269551.

6. Contact: Genoscope

Genoscope - Centre National de Sequencage

7. Tue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

8. Email: seqref@genoscope.cns.fr. Neb: www.genoscope.cns.fr.

18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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primer. Five prime end enriched, double-strand cDNA was
                                                                                                                                                                      TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGTG
                                                                                                                                                                                                                                                                                                             GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG
                                            428 TICCAAGGICCCAGCACCAAGAGACACCCGTITACCIGGGAGCCACGGCAGGCAIGCGGI
                                                                                                  GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG
                                                                              TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGAGCCC
                                                                                                                                                  TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTG
                                                                                                                                                                                                                      TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI017CA07QP1&c=5524.f. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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AUTHORS
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BM925184.1 GI:19375563
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Homo sapiens
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5', mRNA Bequence.
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Matches 773; Conservative
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Contact: Genoscope denoted de Sequencage Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr lst strand cDNA was primed with a NotI-oligo(dI) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAG036ZD06_CS03404_1&c=5524.f
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/note="list strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/organism="Homo sapiens"
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/clone="CS0DI073YD08"
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/lab_host="DHIOB"
/clone lib="MIH MGC 122"
/clone lib="MIH MGC 122"
/clone lib="MIH MGC 122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_l: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female blug, 16 week female spleens. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                    1061 bp mRNA linear EST 12-MAR-2002
.6627603 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5762493
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623 CTGGACTTTGGGCTACATGCTGAACCCTGACCACATGATCCCAGCTGAGCAACCATTGT- 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (basea 1 to 1061)
NIH-MGC http://mgc.noi.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
m column: 22
High quality sequence start: 4
High quality sequence stop: 669.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.8%; Score 652.6; DB 5; 92.8%; Pred. No. 1.9e-181; ive 0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5762493"
                                                                1361
                                                                                                                          702
                                                             1341 CACACCTCTCCCCACTCCAC
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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:4309839"
/tlssue type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/clone=lib="mNHI MGC 48"
/note="Organ: B-cells, Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the blrectionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZaPo-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Pred. No. 2.6e-179;
0; Mismatches 3;
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Best Local Similarity 98.7%;
Matches 693; Conservative
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E. (Labasea I to 808)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Connectium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop; 758.
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  CTGGGCAAATTCAGTCAGAAACAAGGTGGTTCAGCATAGTCCCATATGAAACCAATAAT
                                                                   CAAAACCAGACTATCGAGTCCCCAGATAATGCTCTGCAATTTCGCCTCTATGGCAAGGAC
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                                            CAGGAAACCTTTGGAGCTTTGGACCTTGGGGGAGCCTCTACACAAGTCACTTTTGTACCC
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Homo sapiens
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Search completed: September 21, 2005, 23:22:02 Job time : 4882.93 secs
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                                                                                                                                                                                                                                                                                                University of Washington

Box 358070, Seattle, WA 98195-8070, USA

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Box 326 732 6155

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Email: ted@locke.hs.washington.edu

Similar to GenBank entry S73813 S73813 CD39=lymphoid cell

Similar to GenBank entry S73813 S73813 CD39=lymphoid cell

Similar to GenBank entry S73813 S73813 CD39=lymphoid plane

Similar to GenBank entry S73813 S73813 CD39=lymphoid cell

Similar to GenBank entry S73813 S73813 CD39=lymphoid cell

Encitation (Qualifiers)

Location/Qualifiers
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                                                               Macaca mulatta (rhesus monkey)
Macaca mulatta
Macaca mulatta
Macaca mulatta
Macaca, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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                                                                                                                                                                                        Katze,M.G., Bumgarner,R., Korth,M., Feldman,R., Amjadi,M. and
Holzman,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n 45.7%; Score 624.2; DB 6; Length 673; Similarity 98.4%; Pred. No. 4.2e-173; 62; Conservative 0; Mismatches 8; Indels 3
     MMSP0076_A03 MMSP Macaca mulatta cDNA, mRNA sequence.
                                                                                                                                                                                                                          Expressed sequence tags from Rhesus macaque spleen Unpublished (2002)
Contact: Holzman T
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Matches 66
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Sequence

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Sequence

ALIGNMENTS

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US-08-930-921-2

Sequence 2, Application US/08930921B

Sequence 2, Application US/08930921B

Sequence 2, Application US/08930921B

Sequence 2, Application US/08930921B

GENERAL INFORMATION:
APPLICANT: BEAUDOIN, Adrien R.
TITLE OF INVENTION: THEREOF AND PROCESS OF PROCESS OF PURIFICATION
TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
TITLE OF INVENTION: TATP-DIPHOSPHOHYDROLASES-BEAUDOIN
CURRENT APPLICATION NUMBER: PC7/CA96/00223

CURRENT TILING DATE: 1998-01-02

EARLIER FILING DATE: 1996-04-10

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 1818
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Matches 1321; Conservative 0
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13848, A
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71607, A
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                       GenCore version
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Listing first 45 summaries
                                                                                                                         nucleic search, using sw model
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APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
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            Sequence 1475, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 37,071
RELECHANTION INFORMATION:
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1475:
SEQUENCE CHARACTERISTICS:
LINGTH: 1818 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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Best Local Similarity 99.8
Matches 1321; Conservative
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; CLONE: 9765255
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Query Match
Best Local Similarity 99.8
Matches 1321; Conservative
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ORGANISM: Homo sapiens
   US-09-781-796C-2
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                                                                                                                                          GAGCCTCTACACACACTTTTGTACCCCAAAACCAGACTATGAGTCCCCAGATAATG
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                                        TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTG
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RESULT

GENERAL INFORMATION,
APPLICANT: BEAUDOIN, Adrien R.
APPLICANT: BEAUDOIN, Jean
APPLICANT: BEVIGNY, Jean
APPLICANT: BACH, Fritz H.
APPLICANT: BACH, Fritz H.
APPLICANT: ROBSON, Simon
TITLE OF INVENTION: THEREOF AND PROCESS OF PURIFICATION
TITLE OF INVENTION: THEREOF AND PROCESS OF PRODUCING THEREOF BY RECOMBINANT
TITLE OF INVENTION: TECHNOLOGY
FILE REFERENCE: 92033.90019
CURRENT APPLICATION NUMBER: US/09/781,796C
CURRENT FILING DATE: 1996-04-10
PRIOR FILING DATE: 1996-04-10
PRIOR FILING DATE: 1996-04-10
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PRIOR FILING DATE: 1996-04-10
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FRIOR DATE: 1996 ö 640 773 233 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG 160 293 220 353 280 413 340 473 400 533 460 593 520 653 580 713 GITCAACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG 234 GTTCTTCTCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGAAGTGA TCAGCAACTACCCCTTTGACTTCCAGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTG TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCCAGATAATG GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG GCGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC 294 GCGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTG TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGG AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGA TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGAGCCC Gaps DB 4; Length 1818; ; 0 Indels ., m 96.6%; Score 1319.2; 99.8%; Pred. No. 0; ive 0; Mismatches Sequence 2, Application US/09781796C Patent No. 6800284 GENERAL INFORMATION: 714 641 g G ઠે ö 100 257 160

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Gequence 5457, Application US/09949016

patent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: DOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

PILE REPERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: (60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRESENCE for Windows Version 4.0

SEQ ID NO 5457

LENGTH: 2782
                                                                                                                                                                                                   198 GGTTGACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGGATTGTGCTGGATGCGG
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                                                                                 Score 463.2; DB 4;
Pred. No. 2.3e-144;
0; Mismatches 3;
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                                                                                    Query Match
Best Local Similarity 99.4%;
Matches 465; Conservative
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ORGANISM: Human
; TYPE: DNA
; ORGANISM: Humar
US-09-949-016-2106
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US-09-949-016-5457
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Sequence 2106, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: PSESEQ for Windows Version 4.0

LENGTH: 871
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1434 TGAACCTGACCAACATGATCCCAGCTGAGCAATGTCCCACCTCTCTCCCACTCCCA 1493
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ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATG
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                       Sequence 3. Application US/09240639; Patent No. 6350447; GENERAL INFORMATION:
APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Anna Maria
TITLE OF INVENTION: POLYPEPTIDES AND COMPOSITIONS RELATING TO:
TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
CURRENT APPLICATION NUMBER: US/09/240,639
CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2797
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                                                                                                                                                                                           Query Match
21.3%; Score 291; DB 3;
Best Local Similarity 54.3%; Pred. No. 3.6e-86;
Matches 707; Conservative 0; Mismatches 575
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                              TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (83)..(1669)
OTHER INFORMATION:
      2797
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APPLICANT: Chadwick, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: 28110/36120E
CURRENT APPLICATION NUMBER: US/09/908,510A
CURRENT APPLICATION NUMBER: 09/240,639
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 3
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Patent No. 6759214
GENERAL INFORMATION:
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Patent No. 6780410
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Patent No. 6780410
APPLICANT: Frischauf, Brian Paul
APPLICANT: Frischauf, Anna Maria
APPLICANT: Frischauf, Anna Maria
APPLICANT: Frischauf, Anna Maria
APPLICANT: Frischauf, Anna Maria
APPLICANT: Frischauf, Anna Maria
APPLICANT: Frischauf, Anna Maria
TITLE OF INVENTION: ACIDS
FILE REFERENCE: 28110/36120A
CURRENT APPLICATION NUMBER: US/09/905,744B
CURRENT FILING DATE: 2001-0713
PRIOR FLING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Version 3.1
SEQ ID NO 3
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al Similarity 54.3%; Pred. No. 3.6e-86;
707; Conservative 0; Mismatches 575; Indels
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ORGANISM: Homo Sapiens
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; LOCATION: (83)..(1669)
; OTHER INFORMATION:
US-09-905-744B-3
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| FEATURE:
| NAME/KEY: CDS
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| TTER INFORMATION:
| US-10-107-576-3
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ORGANISM: Homo Sapiens
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                                                                                    TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS FILE REFERNCE: 9598-06
CURRENT APPLICATION NUMBER: US/10/107,660
CURRENT FILING DATE: 2002-03-27
PRIOR PALITING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO SEC ID NOS: 20
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                                ; Sequence 3, Application US/10107660; Patent No. 6780977; GENERAL INFORMATION:
                                                                               Brian Paul
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Matches 707; Conservative
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; LOCATION: (83)..(1669)
US-10-107-660-3
                                                                            APPLICANT: Chadwick, APPLICANT: Frischau
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RESULT 10
US-10-107-576-3
Sequence 3, Application US/10107576
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GTTGCAAAATGAAACAGCAGCTAATGAAGTCCTTGAAAGCATCCAAAGCTACTTCAAGTC 579
                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09905732B
Patent No. 6787328
GENERAL INFORMATION:
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ORGANISM: Homo Sapiens
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; LOCATION: (83)..(16
; OTHER INFORMATION:
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                                                  CCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGAATGCGGGTTCTTC
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                            Gaps
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    Length 2797;
 Score 291; DB 4; Length 27
Pred. No. 3.6e-86;
0; Mismatches 575; Indels
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APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
FILE REFERENCE: 28110/36120B
CURRENT APPLICATION NUMBER: US/09/905,732B
CURRENT APPLICATION NUMBER: 09/240,639
PRIOR APPLICATION NUMBER: 09/240,639
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 32
SOFFWARE: Patentin version 3.1
SEQ ID NO ŝ 227 459 107 279 167 339 228 AAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGATTCCAAG 287 GATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGGAGGAGCCTCAGCAA 407 TICTGGTACCTACATTCTCCCTCCTTCTGCAAGGCTATCATTTCACAGCTGATTCCTG GGAGCACATCCATTCATTGGCAAGATCCAGGCAGCGACGCCGGCTGGACTTTGGGCTA GCCCCAAATACACTTTGAAAAGAGTGGGGAATAGCAGCATAGCCTGGTCTTGGCTA GAGTCAGCTCCCACTGCTGCTCCCAAATTTGATGAGGTATATGCCCGCTCTTACTGCTT CTCAGCCAACTACATCTACCACTTGTTTGTGAACGGTTACAAATTCACAGAGGAGACTTG GGAGGAGATAAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTT 168 GCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTCAGAAAGT 400 CCAAGATGTCCCCAGAGCCTTTGAGGAGTGTATGCAAAAAGTCAAAGGGGCAGGTTCCATC 460 CCACCTCCACGGATCCACCCCCATTCACCTGGAGCCACGGCTGGGATGCGCTTGCTGAG CAAGCAAGAGGTCCTCCCTCCAGGACTGAAGTATGGTATTGTGCTGGATGCCGGGTCTTC 108 TCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAGGCGTGGT 48 CCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGGGTTCTTC Gaps 21; CATGCTGAACCTGACCAACATGATCCCAGCTGAGCAACCATTG 1338 Query Match
21.3%; Score 291; DB 4; Length 27
Best Local Similarity 54.3%; Pred. No. 3.6e-86;
Matches 707; Conservative 0; Mismatches 575; Indels

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tch 21.3%;
al Similarity 54.3%;
707; Conservative (
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; LOCATION: (83)..(1672)
US-09-923-304-3
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Sequence 3, Application US/09923304; Patent No. 6797471; GENERAL INFORMATION:
APPLICANT: KATZ.
APPLICANT: JANG, FENG; FINTH
TILLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS

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Pred. No. 3.6e-86;
0; Mismatches 575; Indels
FILE REFERENCE: UTSC:658US
CURRENT APPLICATION NUMBER: US/09/923,304
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 2797
TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 178, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHARE: PEASESEQ for Windows Version 4.0

LENGTH: 2797
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               AATCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACAC
                                            1054 TTTTGAAGGAACTGGGACCCATCTCTGTGTAAGGAGGAGGTGGCTTCCATATTTGACTT
                                                                                                                                             GGGGGATTTTGGGGCCATTTTCAGCTTTTTACTTTGTGATGAAGTTTTTAAACTTGACATC
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Pred. No. 3.6e-86;
0; Mismatches 575; Indels
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Best Local Similarity 54.3%;
Matches 707; Conservative
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; ORGANISM: Human
US-09-949-016-178
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US-09-949-016-178
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                             813
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GAATGAGGCTGAGAAGATTCTGGCAATGCTCCTGCAGAATTCTCCTACCAAAAACCA
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                                                                                ATTTCGCCTCTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCTATGGGAA
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; Sequence 13848, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
; TILE REPERENCE: CLOO1307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
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llarity 54.3%; Pred. No. 3.6e-86;
Conservative 0; Mismatches 575; Indels 2
                                1296 CATGCTGAACCTGACCAACATGATCCCAGCTGAGCAACCATTG 1338
1471 CATGCTCAGCCTGACCAACCAGATCCCAGCTGAAAGCCCTCTG 1513
                                                                                                                                                                                                                                                                                      APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: 28110/36120C
CURRENT APPLICATION NUMBER: US/09/905,743B
CURRENT APPLICATION NUMBER: 09/240,639
PRIOR APPLICATION NUMBER: 09/240,639
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SSOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                Sequence 3, Application US/09905743B; Patent No. 6828423; GENERAL INFORMATION:
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COTHER INFORMATION:
US-09-905-743B-3
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Matches 707; Conserv
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                                                                                                   Length 46885;
                                                                                               Query Match 19.8%; Score 270.2; DB 4; Length Best Local Similarity 98.9%; Pred. No. 2.8e-78; Matches 272; Conservative 0; Mismatches 3; Indels
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; TYPE: DNA; ORGANISM: Human; FEATURE:; NAME/KEY: misc_feature; LOCATION: (1)...(46885); OTHER INFORMATION: n = A,T,C or GUS-09-949-016-13848
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Sequence 7, Appli Sequence 25, Appl Sequence 19, Appli Sequence 29, Appl Sequence 1475, Ap Sequence 5, Appli Sequence 7, Appli Description US-10-646-308-29 US-10-641-643-1475 US-10-934-998-290 US-09-835-147-5 US-09-835-147-7 US-09-835-147-25 US-09-835-147-1 SUMMARIES B 1365 1437 1464 1599 1599 1818 Length Match 100.0 100.0 97.3 96.6 96.6 96.6 Query 1365 1365 1328 1319.2 1319.2 1319.2 Score 1064597 Result

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GENERAL INFORMATION:

APPLICANT: Maliscewski, Charles R.

APPLICANT: Gayle III, Richard B.

APPLICANT: Gayle III, Richard B.

APPLICANT: Gimpel, Steven D.

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recr

FILE REFERENCE: 2879-US

CURRENT APPLICATION NUMBER: US/09/835,147

CURRENT FILING DATE: 2001-04-13

PRIOR APPLICATION NUMBER: US 60/104,585

PRIOR FILING DATE: 1998-10-16

PRIOR FILING DATE: 1998-11-06

PRIOR PLILING DATE: 1999-10-13

PRIOR PLILING DATE: 1999-10-13

PRIOR PLILING DATE: 1999-08-13

PRIOR PLILING DATE: 1999-10-13

NUMBER: OF SEQ ID NOS: 31

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NOS: 31
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6 US-10-934-998-46
1 US-10-934-998-193
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4 US-10-92-933-304-3
5 US-10-92-933-304-3
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7 US-10-176-982-495
7 US-10-176-995-495
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Patent No. US20020002277A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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Sequence 7, Application US/09835147

Sequence 7, Application US/09835147

Batefit No. US200200277A1

GENERAL INFORMATION:

APPLICANT: Maliszewski, Charles R.

APPLICANT: Gayle III, Richard B.

APPLICANT: Gimel' Steven D.

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2879-US

CURRENT APPLICATION NUMBER: US 60/104,585

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1999-08-13

PRIOR FILING DATE: 1999-08-13

PRIOR APPLICATION NUMBER: PCT/US99/22955

PRIOR APPLICATION NUMBER: PCT/US99/22955

PRIOR PLING DATE: 1999-10-13

NUMBER OF SEQ ID NOS: 31

SEQ ID NOS: 31

SEQUENAL: APPLICATION NUMBER: PCT/US99/22955
ACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGGAGATAAAAACATCTTACGCT
                                                            TITIACTITIGEGARGITITITAAACTIGACATCAGAAAAGTCTCTCAGGAAAAGGTG
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ORGANISM: Artificial Sequence
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Similarity 100.0%; Pred. No. 0;
55; Conservative 0; Mismatches
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US-09-835-147-5
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                                           APPLICANT: Maliszewski, Charles R.
APPLICANT: Gayle III, Richard B.
APPLICANT: Gayle III, Richard B.
APPLICANT: Price, Virginia L.
APPLICANT: Gimpel, Steven D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
FILE REPRENCE: 2879-US
CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT APPLICATION NUMBER: US 60/104,585
PRIOR APPLICATION NUMBER: US 60/107,466
PRIOR FILING DATE: 1998-11-06
PRIOR PLING DATE: 1998-11-06
PRIOR PLING DATE: 1998-11-06
PRIOR PLING DATE: 1998-11-06
PRIOR PLING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR PLING DATE: 1999-10-13
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Sequence 1, Application US/09835147
Patent No. US20020002277A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (67)..(1596)
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llarity 99.8%; Pred. No. 0;
Conservative 0; Mismatches
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; TYPE: DNA
; ORGANISM: Homo 8:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)..
US-10-646-308-29
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Best Local Simi
Matches 1321;
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US-10-646-308-29

Sequence 29, Application US/10646308

Sequence 29, Application Would 13692A1

GENERAL INFORMATION:

APPLICANT: BUTNON, PAUL B. J.

APPLICANT: DEISHER, Theresa A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE

FILE REFERENCE: 3432-B

CURRENT FAPLICATION NUMBER: US/10/646,308

CURRENT FILING DATE: 2003-08-21

PRIOR APPLICATION NUMBER: --to be assigned--

PRIOR APPLICATION NUMBER: --to be assigned--

PRIOR PILING DATE: 2003-08-12

PRIOR PILING DATE: 2003-08-28

NUMBER OF SEO ID NOS: 36

SOFTWARE: Patentin version 3.2

SEO ID NO 29

LENGTH: 1599
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              ; LIBEARY GENDANK
; CLONE: 9762555
; SEQUENCE DESCRIPTION: SEQ ID NO: 1475
US-10-641-643-1475
                                                                                                           Query Match 96.6%;
Best Local Similarity 99.8%;
Matches 1321; Conservative
TOPOLOGY: linear IMMEDIATE SOURCE:
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   GTTACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG 1132
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                                                   ATTTTGGGGCATTTTTACTTTTTTACTTTTGTGATGAAGTTTTTAAACTTGACATCAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cocks, Benjamin G.
Susan G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Word Perfect 6.1 for Windows/MS-DOS
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: «Unknown»
FILING DATE: «Unknown»
APPLICATION NUMBER: «Unknown»
APPLICATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 37,071
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 POLTER DRIVE
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
8-10-641-643-1475
Sequence 1475, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1475:
SEQUENCE CHARACTERISTICS:
LENGTH: 1818 base pairs
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STRANDEDNESS: single
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COUNTRY: USA
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Sequence 290, Application US/10934998

Fublication No. US20050133917A1

GENERAL INFORMATION:

APPLICANT: AL-MAHNNOD, SALMAN

APPLICANT: COLIN, SYLVIE

APPLICANT: SCHNEIDER, CHRISTOPHE

TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL

TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF

TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF

FILE REFERENCE: BMA-04-1206

CURRENT APPLICATION NUMBER: DCT/FR03/00695

PRIOR FILING DATE: 2003-03-04

PRIOR FILING DATE: 2003-03-04

PRIOR PLLING DATE: 2003-03-04

PRIOR PLLING DATE: 2003-03-04

PRIOR PLLING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 301

SOFTWARE: PATENTIN VERSION 3.2

SEQ ID NO 290

LEGGTH: 1818

TYPE: NUM
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 GTTACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCACCACCAGGGGG 1133
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DATABASE ACCESSION NUMBER: Genbank/S73813
FINDAM FOR STATE BOOK 1995-04-12
POS-10-934-998-290
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ORGANISM: Homo
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Sequence 147, Application US/10934998

Sequence 147, Application No. US2005015391741

GENERAL INFORMATION:
APPLICANT: AL-MARMODD, SALMAN
APPLICANT: COLIN, SYLVIE
APPLICANT: COLIN, SYLVIE
TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
FILE REFERENCE: BMA-04-120
CURRENT APPLICATION NUMBER: US/10/934,998
CURRENT FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: PCT/FR03/00695
PRIOR PLING DATE: 2003-03-04
PRIOR PLING DATE: 2002-03-04
PRIOR FILING DATE: 2002-04-11
PRIOR FILING DATE: 2002-04-11
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        APPLICANT: SHIFFMAN, DOV.
APPLICANT: SHIFFMAN, DOV.
APPLICANT: SCHILMAN, Richard M.
APPLICANT: SELLHAMN, Richard M.
APPLICANT: SELLHAMN, Richard M.
APPLICANT: SELLHAMN, SELLHAMS
APPLICANT: PORTER, Gordon J.
APPLICANT: MIKITA, Thomas
APPLICANT: MIKITA, Thomas
APPLICANT: TAI, Julie
ITLE REFERENCE: PA-0025 PCT
CURRENT FILLING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: 60/195,106
PRIOR FILLING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 276
SOFTWARE: PROGRAM
SEQ ID NOS: 276
SEQ ID NO 242
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030165924A1 347965.2
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96.6%; Score 1319.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches
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GENOMICS, INC
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FEATURE:
NAME/KEY: unsure:
LOCATION: 3369
COTHER INFORMATION: a, t, c, US-10-240-965-242
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LENGTH: 4411
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Publication No. US20050153917A1
GENERAL INFORMATION:
APPLICANT: AL-MAHMOOD, SALMAN
APPLICANT: COLIN, SYLVIE
APPLICANT: SCHNEIDER, CHRISTOPHE
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
CURRENT APPLICATION NUMBER: US/10/934,998
CURRENT APPLICATION NUMBER: US/10/934,998
CURRENT FILING DATE: 2004-09-03
PRIOR FILING DATE: 2003-03-04
PRIOR FILING DATE: 2003-03-04
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                                                                                                                                              3; Indels
                                                                                                               Score 640.2; DB 22;
Pred. No. 4.3e-193;
0; Mismatches 3;
                                                                                                                  46.9%;
NUMBER OF SEQ ID NOS: 301
SOFTWARE: Patentin version 3.2
SEQ ID NO 147
LENGTH: 704
                                                                                                               Query Match
Best Local Similarity 99.5'
Matches 642; Conservative
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US-10-934-998-193/c
                                                         TYPE: DNA
ORGANISM: Homo
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Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT Hyseq, Inc.
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                 Score 640.2; DB 22
Pred. No. 1.6e-192;
                                                                                                                                                                                                                                                                                           0; Mismatches
PRIOR FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: FR02/04546
PRIOR FILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 301
SOFTWARE: Patentin version 3.2
SEQ ID NO 193
LENGTH: 6164
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al Similarity 99.5%;
642; Conservative
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US-09-918-995-24656
                                                                                                                                                      TYPE: DNA
CRGANISM: Homo
US-10-934-998-193
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                                                                        50 caccacrccadededarrrrededecarrrrcadcrrrrracrrretaardaadrrrrraa
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80.2%; Pred. No. 7.8e-96;
tive 0; Mismatches 97; Indels 0;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Graff, Jonathon M.
APPLICANT: Muenster, Matthew
TITLE OF INVENTYON: METHODS TO 1DENTIFY SIGNAL SEQUENCES
FILE REFERENCE: A34943 090495.0243
CURRENT APPLICATION NUMBER: US/10/002,631C
CURRENT APPLICATION NUMBER: 05/300,309
PRIOR PAPLICATION NUMBER: 60/300,309
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 275
LENGTH: 703
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; OTHER INFORMATION: n = A, C,
US-10-002-631C-275
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Best Local Similarity 80.2°
Matches 394; Conservative
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ORGANISM: Mus musculus
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US-10-002-631C-275/c
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Fublication No. US20030073623A1
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT PILING DATE: 2001-07-30
FRIOR APPLICATION NUMBER: US/09/235,076
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FRELSE 299-01-20
NUMBER OF SEQ ID NOS: 38054
SEQ ID NO 23052
LENGTH: 484
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                                                                                                                                                                                  Score 414; DB 10;
Pred. No. 6.3e-121;
0; Mismatches 15;
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24656
LENGTH: 475
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LOCATION: (1)...(484)
OTHER INFORMATION: n = A,T,C or G
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96.6%;
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Best Local Similarity 96.6
Matches 423; Conservative
                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-24656
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ORGANISM: Homo sapiens
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US-09-918-995-23052
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467 639 527 669 587 647 813 933

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                     CCAGCCCTTTGACTTTTAGGGGTGCTCAAATCATTTCTGGGCAAGAAGAAGAGGGGTATATGG
                                                              CAGITACTGCCCTTACTCCCAG---TGTGCCTTCAATGGGATTTTCTTGCCACCCCA
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CTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTGCCTATGG
                                                                                                                                                                                         588 TACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATGCTCTGCA
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Job time : 993.919 secs
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 367 ACAGATGAAATCGGTGCGTACCTGGCCGAATGCATGGAACTGTCCACCGAACTGATACCA 308
                                                              ccaagargrececagagecrrrgaggagrerargeaaaagreaagggaggaggreare
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                               AACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTGCCTAT
                                                                                                                                                                                                                                            CCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGGTTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KATZ, RUTH
APPLICANT: JIANG, FENG
TITLE ON INVENTION DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
FILE REFERENCE: UTSC:658US
CURRENT APPLICATION NUMBER: US/09/923,304
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 12
LENGTH: 2797
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                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 3, Application US/09923304; Patent No. US20020081612A1; GENERAL INFORMATION:
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Matches 707; Conservative
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ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (83)..(1672)
US-09-923-304-3
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US-09-923-304-3
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Deficiency of the sequences artificial sequences.

E 1 (bases 1 to 1437)
S Maliazewski, C.R., Tili, R.B.G., Price, V.L. and Gimpe, S.D.
Inhibitors of platelet activation and recruitment
D Patent: JP 2002527096-A 3 27-AUG-2002;
IMMUNEX CORP
OS Artificial Sequence
PD 27-AUG-2002
PP 13-OCT-1999 UP 2000577185
PR 16-OCT-1999 US 60/104585,06-NOV-1998 US 60/107466 PR 13-AUG-1999 US 60/149010
PI CHARLES R MALISZEWSKI, RICHARD B GAYLE III, VIRGINIA L PRICE, PI
AF037366 MUB mUBCU
BC011278 MUB mUBCU
UB1295 Rattus norv
CQ870265 Sequence
AJ33134 Homo sapi
AX828501 Sequence
AX828501 Sequence
BC073267 Xenopus 1
BC07662 Xenopus 1
CQ771824 Sequence
AX82840 Sequence
AJ720369 Gallus ga
BC078240 Danio rer
CQ715235 Sequence
AX562109 Sequence
AK567107 Sequence
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C12N15/09,A61K38/00,A61P9/00,C07K14/705,C12N1/15,C12N1/19,
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Description of Artificial Sequence: Pusion construct of human
CD39
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1437; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibitors of platelet activation and recruitment. BD228700.1 GI:33038470
JP 2002527096-A/3.
Synthetic construct Synthetic construct other semments.
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[1]. (1434).
Location/Qualifiers
1. 1437
/ Arganism="synthetic construct"
//mol type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                   CQ870268
AX813134
AX828511
AX828541
AX828541
BC0772267
BC0772184
AJ720369
BC078240
CQ715235
AR194793
AR567109
AR567207
AR567913
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BD228700
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
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BD228699 Inhibitor
BD228699 Inhibitor
BD228699 Inhibitor
U87967 Human ATP d
AR16835 Sequence
AR380930 Sequence
AR3828644 Sequence
S73813 CD3=1ympho
AK828400 Sequence
CQ870272 Sequence
CQ870272 Sequence
CQ870274 Sequence
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                                                                                                               September 21, 2005, 16:22:35; Search time 6446.5 Seconds (without alignments) 10801.234 Million cell updates/sec
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 (Dases 1 to 1599)
Maliszewski,C.R., Iii,R.B.G., Price,V.L. and Gimpe,S.D.
Inhibitors of platelet activation and recruitment
Patent: JP 2002527096-A 1 27-AUG-2002;
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Location/Qualifiers
                                               אסם 1599 bp DNA linear
Inhibitors of platelet activation and recruitment.
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ive 0; Mismatches
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002527096-A/1.
Homo sapiens (human)
Homo sapiens
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Matches 1321; Conservative
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Beaudoin, A.R., Bach, F.H. and Robson, S.C.
Direct Submission
Submitted (30-JAN-1997) Medicine, Harvard University, 99 Brookline
Avenue, BIDDC, RN, Boston, MA 02215, USA
Location/Qualifiers
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                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1704)
Kaczmarek,E., Koziak,K., Sevigny,J., Siegel,J.B., Anrather,J., Beaudoin,A.R., Bach,F.H. and Robbon,S.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 1704)
Robson,S.C., Kaczmarek,E., Siegel,J.B., Candinas,D., Koziak,K., Millan,M., Hancock,W.W. and Bach,F.H.
Loss of ATP diphosphohydrolase activity with endothelial cell
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31. .1563
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Oy 1433 CCTA 1436 	RESULT 6 AR168353 AR168353 AR168353 AR168353 AR168353 AR168353 AR168353 AR168353 AR168353 AR168353 AR168353 AR168353 AR168353	AR168353.1 GI:17904224	SOURCE Unknown. ORGANISM Unknown: Unclassified. REFERENCE 1 (Dases 1 to 1818)	AUTHORS Beautoli, A.K. and Seviginy, O.  TITLE Mammalian ATP-diphosphohydrolases and process of purification thereof JOURNAL Patent: US 6287831742 11. SEP-2001;	rce	Query Match Query Match Best Local Similarity 99.8%; Pred. No. 0; Marches 13.1: Conservative 0: Mismarches 3: Indels 0; Gabs 0;	TCAACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG 17	173 GITCITCTCACACAGTITATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG 234 GITCITCTCACACACAGTITATACATCTATAAGTGGCCAGCAGAAAAGGAAAAGAAAA	233 GOTGOTGCATCAAGTAGAAGAATGCAGGCTTAAAGGTCCTGGAATCTCAAAATTTGTTC 246 GCCTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC 256 GCCTCCTCAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAA	293 AGAAAGTAAAATGAAATAGCCATTTACCTGACTGACTGCAAGGAAAGGCTAGGAAAGTGA 1	353 TTCCAAGGTCCCAGCACCAAGAACACCCGTTTACTGGGAGCCACGCAGGCATGCGGT 414 TTCCAAGGTCCAAGAACAAGAACACCCGTTTACTGGAACACGCAGGAGCAGGAACACGCAGGAAGAACACCCGTTTACTGGAAGCCAGGAGCAGGAACACACGCCATTAACTGGAAGCAAGAGAACACAGGAAGAACACACGCAAGAACACACACAGAAGCAAGAAAAAA	413 TGCTCAGGATGGAAAGTGAAGAGTTGGCAACAGGGTTCTGGATGTGTGTG	473 TCAGCAACTACCCCTTCAGGGTGCCAGGATCATTACTGGCCAAGGAGGTG 473 TCAGCAACTTTCAGGGTGCCAGGATCATTACTGGCCAAGGAGGTG 53.4 TCAGCAACACACATTCAGGGGGGGGGGGAACATCATTACTGGCCAAGAGAGGAGGTG	533 CCTATGGCTGGATTACTATCAGCTGGGGGAAATTCAGTCAG	593 TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGAGCTTTGGAGCTTTGGAGGTTTTGGACCTTTGGAGGTTTTGGACCTTTGGAGGAGCTTTGGAGGAGAACCTTTGGAGGAGAAACCTTTGGAGAAACCTTTGGAGAAAAAAAA	653 GAGCCTCTACACAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCCAGATAATG		
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Matches   131;   Conservative   0;   Mismatches   3;   Indels   0;   Gaps   0;	293 AGRANGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGA 352	TGCTCAGGATGGAAAGTGAAGGTTGGCAGACAGGGTTCTGGATGTGGTGGAGAGGGGCC TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAGGTG	593 TGAGCATACTCCCATATGAAACCAATAATCAGAAACCTTTGGAGCTTTGGAGCCTTGGGGG 652  [		953 TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACACCA 1012 1014 TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACACCA 1073 1013 GTTACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGG 1072 1074 GTTACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGG 1133 1073 ATTTTGGGGCATTTTCAGCTTTTACTTTGTGATGAAGTTTTTAAACTTGACACATCAGAGA 1132 1134 ATTTTGGGGCATTTTCAGCTTTTTACTTTGTGATGAAGTTTTTAAACTTGACATCAGAGA 1193 1133 AAGTCTCTCAGGAAAAGGTGACTGAAAAAGTTTTTAAACTTGACAGGGG 1193 1194 AAGTCTCTCAGGAAAAGGTGACTGAAAAAGTTCTGTGCTCAGCGTTGGGAGG 1193 1195 AAGTCTCTCAGGAAAAGGTGACTGAAAAAGTTCTGTGCTCAGCCTTGGGAGG 1253
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473 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTG 532	653 GAGCCTCTACACAAGTCACTTTTGTACCCCAAAACCAGACTATCGAGTCCCCAGATAATG 712	ATGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATG 83 ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATG 83 AAATTCTCAGGGACCCATGCTTTCATCCTGGATATAAGAAGGTAGTGAACGTAAGTAA	TCCAGGGTATTTGGAAGTTATCAACATGCCATCAAGGCATCCTGGAGGTCTTCAACACACATCAAGGTTTTTTTT	1133   AAGTCTCTCAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCAGCCTTGGGAGG   1192		RESULT 9 873813 LOCUS 873813 1818 bp mRNA linear PRI 12-APR-1995
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Oy 1193 AGATAAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGGATTTCTG 1252	1373 TGAACCTGACCAACATGATCCCAGCTGAGCAATGTCCACACCTTCTCTCCCG	RESULT 8  AX828644 LOCUS DEFINITION Sequence 290 from Patent W003074073. ACCESSION AX828644.1 GI:39838595 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens	REFERENCE 1  AUTHORS Al-Mahmood, S., Colin, S. and Schneider, C.  TITLE Genes involved in regulating anglogenesis, pharmaceutical preparations containing anglogenesis, pharmaceutical preparations (FR)  FEATURES  1. 1818  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.  //orline Homo.	ORIGIN  Query Match  Query Match  Best Local Similarity 99.8%; Score 1319.2; DB 6; Length 1818;  Best Local Similarity 99.8%; Pred. No. 0;  Matches 1321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  Qy 113 GTTCAACCCACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGGGG 172  Db 174 GGTTGACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGGGG 233	Qy         173 GTTCTTCTCACACAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG         232           HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	413 TGCTCAGGATGGAAAGTGAAGAGTTGGCAACAGGGTTCTGGATGTGCTGGAGAGGAGCCCAGACAGGATGTCAGATGTGATGAAGAGAGAG

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653 652 713 712 773 772 833

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894 AAATTCTCAGGGACCCATGCTTCATCCTGGATATAAGAAGGTAGTGAACGTAAGTGACC 953
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                                                                                                                                                                                                                                                                                TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTG
                                                                                                                         TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG
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CD39=lymphoid cell activation antigen [human, B lymhpoblastoid cell line, MP-1, mRNA, 1818 nt]. 873813
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(bases I to 1818)
Maliszewski,C.R., Delespesse,G.J., Schoenborn,M.A., Armitage,R.J., Fanslow,W.C., Nakajima,T., Baker,E., Sutherland,G.R., The CD39 lymphoid cell activation antigen. Molecular cloning and structural characterization
J. Immunol. 153 (8), 3574-3583 (1994)
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matsumoto, M., Sakurai, Y., Kokubo, T., Yagi, H., Makita, K., Matsui, T., Thitani, K., Fujimura, Y. and Narita, N.
The cDNA cloning of human placental ecto-ATP diphosphohydrolases I and II
FEBS Lett. 453 (3), 335-340 (1999)
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Homo sapiens mRNA for ecto-ATP diphosphohydrolase, isolate C1800.
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ecto-ATPDase I; ecto-ATPDase I; PleA 1 gene.
Homo sapiens (numan)
Homo sapiens
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Submitted (23-FEB-1999) Matsumoto M., Department of Blood
Transfusion Medicine, Nara Medical University, Kashihara,
Nara,634-8522, JAPAN
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                                                                                               Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                Al-Mahmood,S., Colin,S. and Schneider,C.
Genes involved in regulating angiogenesis, pharmaceutical
preparations containing same and applications thereof
Patent: w0 03074073-A 46 12-SEP-2003;
Gene Signal (FR)
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches
                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
             AX828400 2081 bp Sequence 46 from Patent WO03074073. AX828400
                                                                                                                                                                                                                    Location/Qualifiers
                                                       AX828400.1 GI:39838400
                                                                              Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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        CTCTGCAATTTCGCCTCTATGGCAAGGACTACAATGTCTACACACATAGCTTCTTGTGCT
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Novel therapeutic targets in cancer
Patent: WO 2004/073120-8 693 02-SEP-2004;
Sagres Discovery, Inc. (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
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/ product="ecto-ATP diphosphohydrolase I"
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/ db xref="Inibrot/Swiss-Prot:P49961"
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/ db xref="Inibrot-
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/db_xref="taxon:9606"
/tissue_type="placenta"
                                                                                               1. .2081
/gene="PleA 1"
184. .1737
/gene="PleA 1"
/EC_number="3.6.1.5"
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99.8%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                            1382 ACATCCATTCATTGGCAAGATCCAGGGCAGCGACGCCGGCTGGACTTTGGGCTACATGC
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Movel therapeutic targets in cancer
Patent: WO 2004074320-A 697 02-SEP-2004;
Sagres Discovery, Inc. (US)
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Sequence 697 from Patent WO2004074320.
CQ870276
CQ870276.1 GI:519998R0
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/mol_type="unassigned DNA"
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Location/Qualifiers
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in soluble CD39 fusion DNA construct, pIL2LsolCD39.  In soluble CD39; solCD39; human; apyrase activity; platelet activation;  able angina; myocardial infarction; stroke; coronary artery disease;  rrosclerosis; pripheral vascular occlusion; precelampsia; embolism;  riosclerosis; pripheral vascular occlusion; precelampsia; propertian;  nulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;  mulopathy; deep venous thrombosis; DVT; pulmonary embolism; PE;  mulopathy; cerebroprocective; antiatteriosclerotic; anticoagulan;  itant; vasotropic; thrombolytic; inhibitor; interleukin 2; IL2; ds.  bette.	10207; UG-2000 (first entry) nn soluble CD39 fusion DNA construct, pIL2LsolCD3				1 291 26.4 484 9 ACH35840 1 291 20.3 2797 3 AAA96067 2 291 20.3 2797 6 AAD31694 3 291 20.3 2797 6 ABK10350 4 291 20.3 2797 12 ADQ99443 5 291 20.3 2797 13 ADR69172 ALIGNMENTS		ω.	DNA; 143	10207	RESULT 1 AAD00207 ID AAD0
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               ACACAAGTCCCCTTTTGTACCCCCAAAACCAGACTATCGAGTCCCCCAGATAATGCTCTGGAA
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                                                                                                                                                                                               GTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTTGGACCTTGGGGGAGCCTCT
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                                                              TACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTGCCTATGGC
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                                                                                                                                                                                                                                                                                                              The present DNA sequence is a fusion construct pIL2LsolCD19, comprising leader peptide of human interleukin 2 (hIL2), 12 amino acids from the mature N-terminus of hIL2 and soluble CD19 (solCD19) coding region, having apyrase activity. This produces high levels of solCD19 expression and activity in the transfected cells. Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting amagiogenesis. It is useful for the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, cabolism, platelet-associated ischaemic disorders including lung, coronary and cerebral ischaemia, thrombosic disorders including coronary, peripheral and cerebral artery thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion, seconlusion, stenosis or restenosis of blood vessels or stroke
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                             98US-0104585P.
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13-AUG-1999;
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The present sequence is coding region of pIL2SolCD39, a fusion construct encoding sol(soluble)CD39 having apyrase activity. Fusion of 12 amino acids from the N-terminus of mature human IL2 to the solCD39 coding region results in high levels of both expression and activity in the supernatants of transfected cells. This is used in the treatment of unstable angina, myocardial infartation, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemiar dischaemia, thrombosic disorder including coronary strety thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis,
                                                                                                      unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelet-associated isohaemic disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombolytic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; venous thrombosis; peripheral artery thrombosis; coagulopathy; deep venous thrombosis; psripheral artery thrombosis; coagulopathy; deep venous thrombosis; psripheral artery thrombosis; ransient ischaemic attack; thrombus formation; occlusion; stenosis; restenosis; antianginal; cardiant; cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant; coronary ischaemia; vascular occlusion; ss.
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                                                                                         Soluble CD39; ADP-induced platelet activation; platelet aggregation;
                                                                                                                                                                                                                                                                                                                               "Mature human IL2 protein"
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"human IL2 leader sequence"
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                                                              Coding region of pIL2Lsol CD39
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The present DNA sequence is a fusion construct pIL2LFlagSolCD39, comprising the leader peptide of human interleukin 2 (hIL2), 12 amino acids from the mature N-terminus of hIL2, a linker, FLAG tag sequence and soluble CD39 (solCD39) coding region, that has apyrase activity This coluble CD39 (solCD39) is constructed by removing the N- and C-transfected cells. Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting angiogenesis. It is useful for the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, catheroscalerosis, paripheral vascular occlusion, precelampsia, embolism, clatcher-associated ischaemic disorders including coronary and cerebral ischaemic thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis, intracardiac and venous thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE) and thrombosis formation or reformation, occlusion, reocclusion, stenosis or thrombosis 
145. .1461
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Best Local Similarity 98.2%; Pred. No. 0;
Matches 1437; Conservative 0; Mismatches
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98US-0107466P.
99US-0149010P.
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P-PSDB; AAY70921.
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     misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                          CAGGAAAAGGTGACTGAGATGATGAAAAAGTTCTGTGCTCCAGCCTTGGGAGGAGATAAAA 1200
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  901 ACCCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGGCAGTTTGAAATCCAGGGT 960
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/product= "Fusion protein of pIL2LFlagSolCD39"
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/note= "Linker sequence"
121. .144
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/product=
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TGGACTTTGGGCTACATGCTGAACCTGACCAACATGATCCCAGCTGAGCAACCATTGTCC 1413
                                                                                                                                                                                                                                                           Soluble CD39; ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; coronary artery disease; atherosclerosis; peripheral vascular occlusion; preeclampsia; embolism; platelat-associated ischaemia disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombotic disorder; coronary artery thrombosis; cerebral artery thrombosis; intracardiac thrombosis; thrombosis; peripheral artery thrombosis; cosquiopathy; deep venous thrombosis; peripheral artery thrombosis; cosquiopathy; deep venous thrombosis; peripheral artery thrombosis; casquiopathy; deep venous thrombosis; purperipheral artery ambolism; transient ischaemic attack; thrombosis; DVT; occlusion; reocclusion; tenosis; restenosis; antianginal; cardiant; cerebroprotective; antiateriocisclerotic; vasotropic; anticoagulant; coronary ischaemia; vascular occlusion; solCD39 expression plasmid; ss.
              1381 TGGACTTTGGGCTACATGCTGACCTACACATGATCCCAGCTGAGCAACCATTGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein"
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/product= "SolCD39 expression plasmid
                                                                                                                                                                                                                                     region of soluble CD39 expression plasmid.
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*tag= a
note= "huIL2 leader sequence"
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/note= "Flag tag"
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The present sequence is the coding region of soluble CD39(solcD39) expression plasmid. This was used for the transient expression of solCD39 protein in mammalian expression systems. SolCD39 is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, coronary ischaemia and cerebral ischaemia a thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, thrombosis, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PB), transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, recoclusion, stenosis or restenosis of blood vessels or stroke
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mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39 polypeptides.
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Matches 1437; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                               /notes "N-terminus of mature human interleukin 2 (IL2)" 46.\ .1362 /*tags c
                                                                           /*tag= a
/product= "Fusion protein of human Interleukin 2 (IL2)
terminus and human soluble CD39 protein"
                                                                                                                                                                                          /*tag= c
/note= "Coding region of human soluble CD39 (solCD39)"
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100.0%; Pred. No. v.
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                                               cocation/Qualifiers
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98US-0107466P.
99US-0149010P.
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P-PSDB; AAY70913.
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Homo sapiens.
Synthetic.
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06-NOV-1998;
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peripheral artery

artery thrombosis, intracardiac thrombosis,

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ATCCAGGCCAGCGACGCCGGCTGGACTTTGGGCTACATGCTGAACCTGACCAACATGATC 1392
                     The present cDNA sequence is a fusion construct encoding sol(soluble)CD39 having apyrase activity. Fusion of 12 amino acids from the N-terminus of mature human IL2 to the solCD39 coding region results in high levels of both expression and activity in the supernatants of transfected cells. This is used in the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, platelet-associated ischaemic disorder including lung ischaemia, coronary ischaemia and cerebral ischaemia, a thrombotic disorder including coronary artery thrombosis,
                                                                                                                                                                                                                                                                                                                                                     Soluble CD39; ADP-induced platelet activation; platelet aggregation; unstable angina; myocardial infarction; stroke; ocronary artery disease; atherosclerosis; peripheral vascular occlusion; precelampsia; embolism; platelet-associated ischaemic disorder; lung ischaemia; thrombolytic; cerebral ischaemia; thrombosis; cerebral artery thrombosis; intracardiac thrombosis; nerous thrombosis; peripheral artery thrombosis; cogquiopathy; deep venous thrombosis; peripheral artery thrombosis; cagquiopathy; deep venous thrombosis; PB; pulmonary embolism; transient ischaemic attack; thrombus formation; cercebrogrotective; anciarteriosclerotic; vasctropic; anticoagulant; cerebrogrotective; anciarteriosclerotic; vasctropic; anticoagulant; coronary ischaemia; vascular occlusion; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39 polypeptides.
                                                                                               CCAGCTGAGCAACCATGTCCACCTCTCTCCCCACTCCACTAA 1365
                                                                          CCAGCTGAGCAACCATTGTCCACACCTCTCTCCCACTCCACCTAA 1437
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                                                                                                                                                                                                                                                                                                                        Fusion construct of human soluble CD39 cDNA-1.
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(CORR ) CORNELL RES FOUND INC
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The present sequence is the cDNA encoding the human soluble CD39 protein, a cell surface molecule, having apyrase activity. It is derived from a human B cell line cDNA library, referred to as MP-1. Soluble CD39 is constructed by removing the N- and C-terminal transmembrane domains. It retains the capacity to metabolise ATP and ADP at relevant concentrations and the ability to block and reverse ADP-induced platelet activation and recruitment, including platelet aggregation. Soluble CD39 polypeptides are useful for inhibiting anglogenesis. It is useful for the treatment of unstable angina, myocardial infarction, stroke, coronary artery disease or injury, attherosclerosis, peripheral vascular occlusion, precclampsia, embolism, platelet-associated ischaemic disorders including lung, coronary and cerebral ischaemia, thrombotic disorders including coronary, coronary and cerebral artery thrombotic disorders including coronary, thrombosis, intracardiac and venous thrombosis, cosgulopathy, deep venous thrombosis (DVT), pulmonary embolism (PB) and transient ischaemic attack. Soluble CD39 is also useful for preventing thrombus formation or reformation, occlusion, reocclusion,
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                            Example 9; Page 85-87; 122pp; English
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99.8%; Pred
0; F
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Matches 1321; Conservative
                      WPI; 2000-339644/29.
P-PSDB; AAY70910.
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Best Local Similarity
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                      GGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTTTTCTGGTACCTACATTCTCTCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human soluble CD39 protein encoding cDNA
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67. .1599
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The present cDNA sequence encodes soluble CD39 having apyrase activity.

This was derived from a cDNA library prepared from a human B cell line
referred to as MP-1. Soluble CD39 retains the capacity of wildtype CD39

Co metabolise ATP and ADP at physiologically relevant concentrations as
well as the ability to block and reverse ADP-induced platelet activation
and recruitment including platelet aggregation. This is used in the
treatment of unstable angina, myocardial infarction, stroke, coronary
cartery disease or injury, atherosolarosis, peripheral vascular occlusion,
preclampsia, embolism, platelet-associated ischaemic disorder including
coronary ischaemia and cerebral ischaemia, a hrombotic
disorder including coronary artery thrombosis, cerebral artery
thrombosis, intracardiac thrombosis, peripheral artery thrombosis, compliant ischaemia, a thrombosis,
thrombosis, thrombosis, coagulopathy, deep venous thrombosis, venous
thrombosis, thrombosis, cransient ischaemic attack. Soluble CD39 is also
useful for preventing thrombus formation or reformation, occlusion,
tecclusion, stenosis or restenosis of blood vessels or stroke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting platelet activation and recruitment, useful for treating a mammal suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, comprises administering soluble CD39 polypeptides.
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cerebroprotective; antiarteriosclerotic; vasotropic; anticoagulant; coronary ischaemia; vascular occlusion; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.8%; Score 1319.2; DB 3; Length 1599; 99.8%; Pred. No. 0; i.ve 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1599 BP; 446 A; 366 C; 382 G; 405 T; 0 U; 0 Other;
                                                                                                                                                            "Soluble CD39 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maliszewski CR, Gayle RB, Marcus AJ;
                                                                                                   Location/Qualifiers
67. .1599
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(CORR ) CORNELL RES FOUND INC.
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99US-0149010P.
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/product=
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                                                                                                                                                                                                     WO200023094-A2
                                                              Homo sapiens
                                                                                                                                                                                                                                                                                  13-OCT-1999;
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                                                                                                                            ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATG
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4-1BB; CD30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method of treating cardiovascular disease in a subject, comprising administering an IL-17, IL-18, 4-1BB, CD30 or OX40 antagonist. The IL-17, IL-18, 4-1BB, CD30 or OX40 antagonists are useful for treating cardiovascular disorders, e.g. chronic immune) myocarditis, congestive heart failure, aneurysms, angina, embolism, restenosis, ischaemia or thrombocytopenic purpura. T present sequence is a coding sequence used in the exemplification of t
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The invention relates to a conjugate (1) comprising an enzyme and a biodegradable polymer, where (i) enzymatic activity of the enzyme is biodegradable polymer, where (i) enzymatic activity of the enzyme is conjugate than that of the polymer, or (ii) the half life of the enzyme is longer than that of the polymer. The enzyme is longer than that of the cenzyme in the absence of the polymer. The enzyme is longer than that of the conjugate. The enzyme is a multimeric, soluble and/or extracellular mazyme, colymer. The enzyme especially a soluble form of CD39 and catalyzes hydrolysis of nucleoside diphosphate. The conjugate can be used to treat abnormal aggregation of platelets, particularly cardiovascular disease.

C diseases relating to abnormal levels of extracellular nucleotides or abnormal aggregation of platelets, particularly cardiovascular disease, cancer, sepsis or a disease related to graft transplant. (1) is also used infarction, unstable angina, atherosclerosis, pre-eclampsis, embolism, claraction, unstable angina, atherosclerosis, pre-eclampsis, embolism, clasorders, and thrombosis and coagulopathies associated with exposure to a foreign or injured tissue surface, in combination with angioplasty, carctid endarterectomy, anastomosis of vascular grafts and chronic cardiovascular devices. The present sequence represents a DNA encoding a New enzyme polymer conjugate used for treating abnormal levels of extracellular nucleotides or platelet aggregation, graft transplant, cardiovascular disease, cancer and sepsis. CD39; nucleoside diphosphate; thrombolytic; anticoagulant; cardidovascular; cytostatic; antibacterial; immunosuppressive; cardiant; antianginal; antiarteriosclerotic; gynaecological; cerebroprotective; cancer; human; apyrase; gene; de.

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AAGTCTCTCAGGAAAAGGTGACTGATGATGATGAAAAGTTCTGTGCTCAGCCTTGGGAGG 1216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated ATP di:phospho:hydrolase enzymes - have anti-haemostatic
activity, useful for reducing platelet aggregation and thrombogenicity
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                              Sequence 1704 BP; 468 A; 392 C; 403 G; 441 T; 0 U; 0 Other;
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0; Mismatches
                                                    Query Match
Best Local Similarity 99.8%;
Matches 1321; Conservative
      polypeptide.
      human CD39
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          1074 GTTACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG
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II have not been obtained yet. Assuming that the CD39 gene product is an ATPDase type II, the use of CD39 in the reduction of platelet aggregation and of thrombogenicity may be contemplated, as well as a process of making ATPDases using the CD39 sequence (AAT38516)
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                                                                                                                                                                     Query Match 91.8%; Score 1319.2; DB 2; Length 1818; Best Local Similarity 99.8%; Pred. No. 0; Matches 1321; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                          Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;
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                               GTTACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG
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                                                                              Non-human transgenic or somatic recombinant mammals, whose cells contain a heterologous DNA encoding a polypeptide (especially human CD39 protein) having ATP-diphosphohydrolase activity under cellular activating conditions is claimed. In particular the animal is a pig and its cells (or tissues or organs) can be used for transplantation. DNA coding for human CD39 is also useful for genetically modifying a mammalian cell to render it less susceptible to an inflammatory or immunological stimulus and platelet aggregation. The modified cells can be used to prevent or alleviate a thrombotic condition. The present sequence encodes human CD39 protein and was disclosed in J.Immunol. 153 (8) (1994) 3574-3584
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Pred. No. 0;
0; Mismatches 3; Indels 0;
preventing or alleviating thrombotic condition in
                                                                                                                                                                                                                                                                   Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;
                                                Claim 3; Page 38; 65pp; English
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A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma or osteoarthritis.

SEQ ID NO 1475; SOpp; English.

The invention relates to a composition comprising a plurality of CDNAs response. The invention also relates to a method of diagnosing or response. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic conditions to form one or more hybridisation complexes, detecting the nucleic conditions to form one or more hybridisation complexes, detecting the hybridisation complexes and comparing the levels of the detected in a non-diseased sample, where an altered level of the detected hybridisation complexes with the level of hybridisation complexes with the level of hybridisation complexes with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and condition. Also disclosed are an expression profile comprising an immunopathology, such as crohn's disease, asthma, are useful as hybridisable array elements in a microarray for monitoring the diagnosis of an immunopathology, such as Crohn's disease, asthma, culcerative colitis, hypereosinophila, irritable bowel syndrome, colecoarthritis rheumatoid arthritis or acute monocytic leukaemia, and in identifying agents for the treatment of the diseases. The microarray may also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition may also be used in drug discovery and development, toxicological and carcinogenic fragments. This sequence represents a human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed appear of the printed payer of the printed payer. from USPTO at segdata.uspto.gov/seguence.html

Sequence 1818 BP; 494 A; 418 C; 433 G; 473 T; 0 U; 0 Other;

g 요 ò g 셤 **EXEXEXEX** ò ò ò g ò g ö 233 232 353 352 413 412 472 592 GTTCAACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGGATTGTGCTGGATGCGG 172 473 533 593 653 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGTG GTTCTTCTCCACACACTTTATACATCTATAAGTGGCCAGCAGAAAGGAGAATGACACAG GTTCTTCTCACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAG GCGTGGTGCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC GCGTGGTGCATCAAGTAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGA AGAAAGTAAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGA TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGGAGCC TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGTG Gaps 91.8%; Score 1319.2; DB 11; Length 1818; 99.8%; Pred. No. 0; ö Indels 3; 0; Mismatches Best Local Similarity 99.8 Matches 1321, Conservative Query Match 113 174 173 234 233 294 293 354 414 474 534 594 353 473 533 413 ઠે 요 Š g ઠે g g В g ò ઠે ઠ ద

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                                                                                                                                                                                                                                                                                                                                                                                           Compositions for diagnosing, prognosing and treating angiogenic disorders including tumor vascularization and heart disease, comprise nucleic acid or polypeptide differentially expressed in angiogenesis.
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antiinflammatory; cardiant; angiogenesis inhibitor; gene therapy; angiogenesis; endothelial cell; diagnosis; tumor vascularization; retinopathy; rheumatoid arthritis; Crohn's disease; atherosclerosis.
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.8%;
Matches 1321; Conservative
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                                                                                                                     BP141351
BP157197
AGENCOURT
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BP434198
AGENCOURT
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                                                                                                                        BP141351
BP157197
BP171197
BP171611
BP437681
BP434084
BP434198
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Pred. No. 1.4e-302;
0; Mismatches 4;
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AL552087
BX402315
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HTC; CNSLT cDNA.
Homo sapiens (human)
Homo sapiens
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KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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                                                                                                                                                              BX436692 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP003YK21 S-PRIME, mRNA sequence.
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                   1206 GTACCTACATTCTCTCCCTCCTTCTGCAAGGCTATCATTCACAGGCTGATTCCTGGGAGG
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This sequence belongs to sequence cluster 5524.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOCAP003AF11QP1&c=5524.f.
Location/Qualifiers
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The FANTOW CONDITION and the KIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs

Mature 420, 563-573 (2002)

& Adachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, C., Matsuyama, T., Myazaki, R., Sakai, C., Sakai, K., Sakai, K., Sakai, C., Sakai, K., Sakai, C., Sakai, K., Sakai, C., Sakai, K., Sakai, C., Sakai, K.,                                                                                                                                                                                                                                                                                                                                                                      Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. SHIKIN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
    Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                     Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramedeuu, M. and Hayabizaki, Y. Normalization and subbraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new g Genome Res. 10 (10), 1617-1630 (2000)
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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                                              Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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/mol_type="mRNA"
/strain="C57BL/6J"
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URL:http://fantom.gsc.riken.jp/
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Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330437E10 product:ectonucleoside triphosphate diphosphate 1, full insert sequence.
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CAATICCGICTCIAIGGCGAGGACTAIACIGIGIACACACACAGGTICCIGIGCIAIGGG 880
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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High-efficiency full-length cDNA
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SLLQGYNFTDSSWRGIHFWGXLKDSNAGWTLGYMLNLTNMIPAEQPLSPPLPHSTYIG
LMVLFSLLLVANAITGLFIYSKPSYFWKEAV"
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79.8%; Pred. No. 3.5e-243;
ive 0; Mismatches 255;
   /db_xref="FANTOM_DB:4921511C05"
/db_xref="taxon:10090"
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                                                               /sex="male"
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ENVKYGI VLDAGSSHTNLYI YKWPAEKENDTGVVQQLEECQVKGPGI SKYAQKTDEI G
XYLAEKMELSTELI PTSKHYOPVYLAATAGNELANBESGABEVLAAVSTSLKSYP
PDFGGAK II TGYEEAYGWI II NYLLIGRFTOBQSWLSL I SDSGKQETFGAL DLGGGAST
OI TFVPQNSTI ESPENSLQFRLYGEDYTVYTHSPLCYGKDQALWQKLAKDI QVSSGGV
                                                                                                                                                                                                                                                                                          LKDPCFNPGYEKVVNVSELYGTPCTKRFEKKLPFDQFRIQGTGDYBQCHQSILELFNN
STPCYSQCARNGYFLPPLHGSPGAFSAFYFVNDPFKKVAKNSVISQEKNTEITKNRCS
KSWBETKTSYPSVKEKYLSBYGSGAYILSLLQGYNFTDSSWGQIHFMGKIKDSNAGW
TLGYMLNLTNNIPABOPLSPPLPFSYIGLMVLFSLLLUAAVAITGLFIYSKPSYFWKE
                                                                                           /proteIn_id="BAC27039.1"
/db_xref="GI:26326591"
/translation="MEDIKDSKVKRPCSKNILJILGFTSILAVIALIAVGLTQNKPLP
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79.8%; Pred. No. 4.3e-243;
iive 0; Mismatches 255;
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CONAs

Nature 420, 563-573 (2002)

E (bases 1 to 4198)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Haragaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Katoh, H., Kawai, J., Kolini, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kolini, Y., Itoh, M., Magawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kolina, Y., Kondo, S., Konno, H., Kowai, M., Ohsato, N., Okazaki, Y., Satito, R., Satito, R., Satitoh, H., Sakai, K., Sakai, K., Sakaich, Sano, H., Sakait, T., Sakai, T., Sakai, K., Sakait, T., Sakai, K., Shinagawa, A., Shiraki, T., Sagabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A., Direct Submission
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshikagi, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer General Connec Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, UKL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="pituitary gland"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a full-length mouse cDNA collection
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triphosphate diphosphohydrolase 1 (MGD|MGI:102805,
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Please visit our web site for further details.
URL:http://ganome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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db_xref="taxon:10090"
clone="5330437E10"
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/strain="C57BL/6J"
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Nature 409, 685-690 (2001)
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                                                                                                                                                                                                                        >
                                                                                                                             /clone="CSODIO73YD08"
/tissue type="PLACENYA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENYA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-estrand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                                                                                                                            56.5%; Score 812.4; DB 5; 99.2%; Pred. No. 2.3e-228; iive 0; Mismatches 3;
                                                          1. .861
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/mol_type="mRNA"
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                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                     Similarity
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: Beqrefégenoscope.cns.fr. Web: www.genoscope.cns.fr
Estand CDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
For more information about this cluster, see
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8371889 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
Clone CSODI073YD08 3-PRIME, mRNA sequence.
BX371889
                                                                                                                                                                                                                                                                                                    GGGGCATTTTCAGCTTTTTACTTTGTGATGAAGTTTTTAAACTTGACATCAGAGAA---- 1133
                                                                                                                                                                                                                                                                                                                                      121 GTCATCTCTCAGGAGAAATGACCGAGATAACAAAAATTTTTGCTCAAAATGTTGGGAA 1280
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                                                                                                               981 GSCACTCCCTGCACAAAGATTCGAAAGAAGCTACCATTTGATCAGTTTCGAATCCAG 1040
                                                                                                                                                                                        1041 Gecacricaagacracgaacagreccaccagagcarccrrcaagcrerrcaacaacaacacac 1100
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                            CTTAAGGACCCATGCTTTAACCCAGGATACGAGAAGGTTGTGAATGTAAGTGAGCTCTAT 980
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                  1101 TGCCCTTACTCCCAGTGTGCCTTCAATGGCGTCTTCCTGCCACCTCTCCATGGGAGTTTT
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                                                                               898 AAGACCCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAATCCAG
                                                                                                                                                     GGTATTGGAAACTATCAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACACCCAGTTAC
                                                                                                                                                                                                                              TGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGGATTTT
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li,w.B., Gruber,C., Jessee,J. a
Full-length cDNA libraries and
Unpublished (2001)
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On May 8, Zour
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TITLE
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OGYNFTGSSWEQIHPMGKIKDSNAGWTLGYMLNNTNNIPAEQPLSPPLPHSTYIGLMV
LFSLLLVAVAITGLFIYSKPSYFWKEAV"
                                    Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="skin"
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                                                                                                                                                                                                cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTGTCCACCGAACTGATACCAACATCCAACACCACACACTCCTGTCTACCTGGGAGC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 TGGACAAGAGGAGGTGCCTATGGGTGGATTACTATTAACTATCTGCTGGGCAGATTCAC 301
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                The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AATCTCAAAATATGCTCAGAAACAGATGAAATCGGTGCGTACCTGGCCGAATGCATGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IndelB
             Submitted (16-JUL-2001) Yoshihide Hayashizaki,
                                                                                                                                                                                                                                                                                                         prepare mouse tissues.
Please visit our web site for further details.
URL-http://genome.gsc.riken.jp/
URL-http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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/strain="CS7EL/6J"
/db_xref="FANTOM DB:4732419M16"
/db_xref="taxon:10090"
/clone="4732419M16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.7%; Score 743.4; DB 3;
79.2%; Pred. No. 9.8e-208;
iive 0; Mismatches 231;
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Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732419M16 product:ectonucleoside triphosphate diphosphoydrolase 1, full insert sequence.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases I to 3563)
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-langth to CDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSDORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO73YD08"
/tissue type="HACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NorI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
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sites of the pCMVSPORT 6 vector. Library was normalized."
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length CDNA libraries and normalization Unpublished (2001)
On Fe 2001 this sequence version replaced Contact: Genoscope Genoscope - Centre National de Sequencage
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 897)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Will-length CDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31273939.
               305 GCGTGCTCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCAAAATTTGTTC
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
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E 1 (Dasses 1 to 1066)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: LLANLST14 row: c column: 20

High quality sequence stop: 664.

Location/Qualifiers
                                                                                                                                                                                                                        AGENCOURT 6621802 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:S724619
5', mRNA Sequence.
                                         830
              772
                                                                      832
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                                                                                     GTTCAACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG 172
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                          ATGGGAAGGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATG
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Pred. No. 4.6e-203;
0; Mismatches 45; Indels 11;
                                                                                                                                                                                                                                                                                             BM906668.1 GI:19357047
EST.
                                                                                                                                               AAATTCTCAGGGACC 847
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                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
Homo sapiens
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Best Local S:
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1025 bp mRNA linear EST 28-APR-2004
BX402316 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI017YB13 5-PRIME, mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1025)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30610946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="Piacenta COT 25-NORMALIZED"
/clone_lib="Homo sapiens Placenta COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                         AAATTCTCAGGGACCCATGCTTTCATCCTGGATATAAGAAGGTAGTGAACGTAAGTGACC
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                                                                                 For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS1AI005ZB07QP1&c=5524.f. Location/Qualifiers
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Pred. No. 9.9e-196;
0; Mismatches 3;
                                                                                                                                                             893 TTTACAAGACCCCCTGCACCAAGAGATTTGA 923
                                                                                                                                                                                                              867 TTWMAARMCCCCCCMCMARARATTTARATGA 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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99.6%;
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  Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and SCOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.1%; Score 720.6; DB 1; Length 897; 94.3%; Pred. No. 3.4e-201;
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                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens
Homo sapiens
Bukaryotas, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
1 (bases 1 to 952)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                      GTTCTTCTCACACAGAGTTTATACATCTTATWAGTGGCCAGCAGAAAAGGAGAATGACACAG
                                                                                                                                                                                                                                                               368 AGAAAGTAAATGAMATAGGCATTTACCTGACTGATTGCMTGGAAAGAGCTAGGAAGTGA
                                                                                                                                       TGCTCAGGATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGGGGGCC
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Pred. No. 2.3e-194;
5; Mismatches 5;
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nes 697; Conservative
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1 (base 1 to 1023)

2 Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

3 Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

4 Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31269551.

Contact: Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL547722

1023 bp mRNA linear EST 25-MAR-2004
L6147722 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI017YB13 5-PRIME, mRNA sequence.
AL547722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="CSODIO177813"
/tissue type="PLACENTA COT 25-NORWALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="lst strand clona was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
                                                                                          TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTTGGGG
                           TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGAAGGTG
                                                                                                                                                                                                                      TCAGCATAGTCCCATATGAAACCAATAATCAGGAAACCTTTGGAGCTTTGGACCTTGGGG
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/db_xref="taxon:9606"
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Homo sapiens
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AL547722
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292 GCCAGGATCATTACTGGCCAAGAGGAAGGTGCCTATGGCTGGATTACTATCAACTATCTG 351
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/db_xref="taxon:9606"
/clone="IMAGE:5762493"
                                                     1413 CACACCTCTCTCCCACTCCAC 1433
                                                                                 682 CACACCTGTCTTCCACTCCAC
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                Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequescope.cns.fr. Web. : www.genoscope.cns.fr. web.
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                    For more information about this cluster, see http://www.genoscope.cns.fr/cdna?8=CSOBAG036ZD06_CS03404_1&c=5524.f
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Pred. No. 2.6e-182;
0; Mismatches 8;
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/organism="Homo sapiens"
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/lab_host="DH108"
/clone lib="NNH MGC 122"
/clone lib="NNH MGC 122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_l: Not1; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                           1061 bp mRNA linear EST 12-MAR-2002
6627603 NIH_MGC_122 Homo sapiens CDNA clone IMAGE:5762493
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NIH MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Londbulished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Biocesience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12812 row: m column: 22

High quality sequence start: 4

High quality sequence start: 4

High quality sequence stop: 669.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1061)
623 CTGGACTTTGGGCTACATGCTGAACCCTGACCACATGATCCCAGCTGAGCAACCATTGT-
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352 622

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/mol_type="mRNA"
/db xref="laxon:9606"
/clone="InAGE:4309839"
/tissue type="primary B-cells from tonsils (cell line)"
/tissue type="primary B-cells from tonsils (cell line)"
/tissue type="primary B-cells from tonsils (cell line)"
/tissue type="primary B-cells"
/tlab_host="DH10B (phage-resistant)"
/clone=lib="NH1 MGC 48"
/note="Organ: B-cells, Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCAAGGCTATCATTTCACAGCTGATTCCTGGGAGCACATCCATTTCATTGGCAAGATC 1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTACCCCAAAACCAGACTATCGAGTCCCCAGATAATGCTCTGCAATTTCGCCTCTATGGC
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Pred. No. 6.6e-179;
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B. (bases 1 to 808)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be http://image.llnl.gov

Plate: LLCM1183 row: n column: 16

High quality sequence stop; 758.
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  CTGGGCAAATTCAGTCAGAAACAAGGTGGTTCAGCATAGTCCCATATGAAACCAATAAT
                                                                       CAAAACCAGACTATCGGGTCCCCCAGATAATGCTCTGCAATTTCGCCTCTATGGCAAGGAC
                                                                                                                                                                                                                                                                        TACAATGTCTACACACATAGCTTCTTGTGTGTGTGGGAAGGATCAGGCACTCTGGCAAAA
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Homo sapiens
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BF664417
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

DEFINITION

RESULT 14 BF664417

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PEATURES

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                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
1 (bases 1 to 673)
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                                                                                                                                                             Katzz,M.G., Bumgarner,R., Korth,M., Feldman,R., Amjadi,M. and Holzman,T.
Expressed sequence tags from Rhesus macaque spleen
Unpublished (2002)
Contact: Holzman T
                                                                                                                                                                                                                                                          University of Washington
Box 158070, Seattle, WA 98195-8070, USA
Tel: 206 712 6156
Fax: 206 712 6055
Email: ted@locke.hs.washington.edu
Similar to GenBank entry 873813 873813 CD39=lymphoid cell
activation antigen [human, B lymhpoblastoid cell line, MP-1,
1818 nt]. 4/1995
Flate: MMSP0076 row: A column: 03.
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     MMSP0076_A03 MMSP Macaca mulatta cDNA, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                    1. .673
/organism="Macaca mulatta"
/mol_type="mRNA"
/db xref="taxon:9544"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                         ISP0076 row: A column: 03.
Location/Qualifiers
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/clone_lib="MMSP"
/note="Organ: spleen"
                                                             Macaca mulatta (rhesus monkey)
Macaca mulatta
                    CB553295 GI:31302490
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Matches 662; Conservative
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Matches 1321; Conservative
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ORGANISM: Unknown
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Sequence 2, Application US/08930921B

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Sequence 2, Application US/08930921B

Sequence 3, Applicant: BEAUDOIN, Adrien R.

APPLICANT: BEAUDOIN, Adrien R.

TITLE OF INVENTION: THEREOF AND PROCESS OF PROCESS OF PURIFICATION

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THEREOF THE REFERENCE: 1998-01-02

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EARLIER APPLICATION NUMBER: PCT/CA96/00223

SEALIER APPLICATION NUMBER: PCT/CA96/00223

SOFTWARE: PALENTING DATE: 1998-04-10

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PALENTING DATE: 1998-04-10

SEQ ID NO 2

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                                                                                 Sequence 71597, A Sequence 1159, App Sequence 159, App Patent No. 5210029 Patent No. 5464939 Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Patent No. 5314995 Patent No. 5314995 Patent No. 5314995
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US-08-184-009-159

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFTCATION:
PRIOR APPLICATION:
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          Sequence 1475, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Sailhamer
TITLE OF INVENTION: COMPOSITION FOR THE;
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, IN
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1475:
SEQUENCE CHARACTERISTICS:
LENGTH: 1818 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER:
                                                                                                                                                                                                                     CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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HANDIATE SOURCE:

LIBRARY: GENBANK

CLONE: 9765255

US-09-023-655-1475
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CLASSIFICATION:
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PROCESS OF PURIFICATION PRODUCING THEREOF BY RECOMBINANT
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                                APPLICANT: SEVIGNY, Jean
APPLICANT: SEVIGNY, Jean
APPLICANT: SEVIGNY, Jean
APPLICANT: BAGUDOIN, Jean
APPLICANT: BAGUENY, Jean
TITLE OF INVENTION: Simon
TITLE OF INVENTION: THEREOF AND PROCESS OF PROF
TITLE OF INVENTION: THEREOF AND PROCESS OF PROF
TITLE OF INVENTION: TECHNOLOGY
FILE REFERENCE: 92033.900.9
CURRENT APPLICATION NUMBER: US/09/781,796C
CURRENT APPLICATION NUMBER: 08/419,204
PRIOR APPLICATION NUMBER: 08/419,204
PRIOR FILING DATE: 1995-04-10
PRIOR FILING DATE: 1996-04-10
PRIOR FILING DATE: 1996-04-10
PRIOR FILING DATE: 1998-02-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NO. 2.2
                                                                                                                                                                                                                                                                                                                                    91.8%; Score 1319.2;
99.8%; Pred. No. 0;
ive 0; Mismatches
Sequence 2, Application US/09781796C Patent No. 6800284 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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 TCAGCAACTACCCCTTTGACTTCCAGGGTGCCAGGATCATTACTGGCCAAGAGGTG
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is Sequence 5457, Application US/09949016

patent No. 681239

igeneral information:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOON OF 06/241, 755

PRIOR APPLICATION NUMBER: 06/241, 755

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

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PRIOR FILING DATE: 2000-10-0
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                                                                                      Length 871;
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Pred. No. 7e-86;
0; Mismatches 575; Indels
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                                                                                      Score 463.2; DB 4;
Pred. No. 6.7e-144;
0; Mismatches 3;
                                                                                         32.2%;
99.4%;
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Best Local Similarity 54.3%;
Matches 707; Conservative (
                                                                                                                                        465; Conservative
                                                                                      Query Match
Best Local Similarity
Matches 465; Conserv
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; ORGANISM: Human
US-09-949-016-5457
  ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2106
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; Bequence 2106, Application US/09949016
; Bettent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTHARE: PSELSEQ for Windows Version 4.0
; SSO ID NO 2106
LENGTH: 871
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Facent No. 6350447
GENERAL INFORMATION:
APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Anna-Maria
ITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
ITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
FILE REFERENCE: 9598-066
CURRENT PAPLICATION NUMBER: US/09/240,639
CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2797
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                                                                                                                                                                                                                   Score 291; DB 4; Length 2797;
Pred. No. 7e-86;
0; Mismatches 575; Indels 2
                                                                                                                                                                                                                        20.3%;
54.3%;
                                                                                                                                                                                                                        Query Match
Best Local Similarity 54.3
Matches 707; Conservative
; LENGTH: 2797
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (83)..(1669)
; COTHER INFORMATION:
US-09-908-510A-3
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; Patent No. 6/592104;
GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: ACIDS
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120E
; CURRENT FILING DATE: 2010-07-13
PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin version 3.1
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TYPE: DNA

ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
J. LOCATION: (83)..(1669)
CTHER INFORMATION:
US-10-107-576-3
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                        Sequence 3, Application US/10107660

| Sequence 3, Application US/10107660
| Patent No. 6780977
| GENERAL INFORMATION:
| APPLICANT: Chadwick, Brian Paul
| APPLICANT: Chadwick, Brian Paul
| APPLICANT: Frischauf, Anna-Maria
| TITLE OF INVENTION: WETHODS AND COMPOSITIONS RELATING TO CD39-LIKE
| TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
| FILE REFERENCE: 9598-066
| CURRENT APPLICATION NUMBER: US/10/107,660
| PRIOR FILING DATE: 1998-01-29
| NUMBER OF SEO ID NOS: 29
| SOFTWARE: Patentin Ver. 2.0
| SEO ID NO 3
| LENGTH: 2797
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                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (83)..(1669)
US-10-107-660-3
                   US-10-107-660-3
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APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND 1TITLE OF INVENTION: ACIDS
FILE REFERENCE: 28110/36120H
CURRENT APPLICATION NUMBER: US/10/107,576
CURRENT FILING DATE: 1099-01-29
PRIOR FILING DATE: 1999-01-29
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GGATCAGGCACTCTGGCAGAAACTGGCCAAGGACATTCAGGTTGCAAGTAATGAAA---T
                                                                                                                                                GAATGAGGCTGAGAAGATTCTGGCAATGCTCCTGCAGAATTCTCCTACCAAAAACCA
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US-10-107-576-3
Sequence 3, Application US/10107576
Patent No. 6783559
GENERAL INFORMATION:
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SEQ ID NO 3
LENGTH: 2797
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GTTGCAAAATGAAACAGCAGCTAATGAAGTCCTTGAAAGCATCCAAAGCTACTTCAAGTC 579
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20.3%; Score 291; DB 4; Length 27
Best Local Similarity 54.3%; Pred. No. 7e-86;
Matches 707; Conservative 0; Mismatches 575; Indels
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; Patent No. 6787328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                                                                                                          ; GENERAL INFORMATION:
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LOCATION: (83)
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 Score 291; DB 4; Length 2797;
Pred. No. 7e-86;
0; Mismatches 575; Indels 2
20.3%;
al Similarity 54.3%;
707; Conservative
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APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Brian Paul
APPLICANT: Frischauf, Anna Maria
APPLICANT: Frischauf, Anna Maria
TILE OF INVENTION: WETHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND FILE REFERENCE: 28110/36120B
CURRENT APPLICATION NUMBER: 08/09/905,732B
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 09/240,639
PRIOR APPLICATION NUMBER: 09/240,639
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1 TTCTGGTACCTACATTCTCTCTCTCTGCAAGGCTATCATTTCACAGCTGATTCCTG 1307 GCCCCAAATACACTTTGAAAAAGAAGTGGGGAATAGCAGCATAGCCTGGTCTCTTGGCTA 1470 279 239 299 359 459 419 GATGGAAAGTGAAGAGTTGGCAGACAGGGTTCTGGATGTGGTGGAGGAGGAGCCTCAGCAA 479 GAGTCAGCTCCCACTGCTGCTCCCCAAATTTGATGAGGTATATGCCCGCTCTTACTGCTT GGAGGAGATAAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTGAGTGAATACTGCTT GGAGCACATCCATTTCATTGGCAAGATCCAGGGCAGCGACGCCGGCTGGACTTTGGGCTA 240 GCATCAAGTAGAAGAATGCAGGGTTAAAGGTCCTGGAATCTCCAAAATTTGTTCAGAAAGT 340 CAGTCAAACCTTCAAATGTAGTGTGAAAGGCTCTGGAAATCTCCCAGCTATGGAAATAACCC 220 CAAGCAAGAGGTCCTCCCTCCAGGACTGAAGTATGGTATTGTGCTGGATGCCGGGTCTTC 180 TCACACAAGTTTATACATCTATAAGTGGCCAGCAGAAAAGGAGAATGACACAGGCGTGGT 300 AAATGAAATAGGCATTTACCTGACTGATTGCATGGAAAGAGCTAGGGAAGTGATTCCAAG ccaagargiccccagagccrirgaggagrigrarigcaaaagrcaaggggggggriccarc GTCCCAGCACCAAGACACCCGTTTACCTGGGAGCCACGGCATGCGTTGCTCAG ccaccrccacegarccaccccarrcaccreegasccacegeregearecerrecreae 120 CCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGGGTTCTTC Gaps

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tch 20.3%; Score 291; DB 4; al Similarity 54.3%; Pred. No. 7e-86; 707; Conservative 0; Mismatches 575.
          CURRENT APPLICATION NUMBER: US/09/923,304
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
FILE REFERENCE: UTSC:658US
                                                                        LENGTH: 2797
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                       .. (1672)
                                                                                                                                                                            Query Match
Best Local Similarity
Matches 707; Conserv
                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (83)
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; Sequence 3, Application US/09923304
; Patent No. 6797471
; GENERAL INFORMATION:
; APPLICANT: KATZ, RUTH
; APPLICANT: JIANG, FENG
; TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
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Sequence 178, Application US/09949016

Sequence 178, Application US/09949016

SERVERAL INFORMATION:

APPLICATION UNENTION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PELING DATE: 2000-10-3

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 19-08
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Pred. No. 7e-86;
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ORGANISM: Human
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US-09-949-016-178
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US-US-39-ULLIBSURE

Sequence 13849, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WIMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASESEQ for Windows Version 4.0

LENGTH: 46885
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                                                                                                                                         GGATCAGGCACTCTGGCAGAACTGGCCAAGGACATTCAGGTTGCAAGTAATGAAA---T
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US-09-949-016-13848
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                                           1471 CATGCTCAGCCTGACCAACCAGATCCCAGCTGAAAGCCCTCTG 1513
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Pred. No. 7e-86;
0, Mismatches 575; Indels
                                                                                                                                                                                                                APPLICANT: Chadwick, Brian Paul
APPLICANT: Chadwick, Anna Maria
APPLICANT: Erischauf, Anna Maria
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: ACIDS
FILE REFERENCE: 28110/36120C
CURRENT APPLICATION WUMBER: 08/09/905,743B
CURRENT FILING DATE: 1999-01-07-13
PRIOR APPLICATION NUMBER: 09/240,639
PRIOR APPLICATION NUMBER: 09/240,639
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
                                                                                                                                                            Sequence 3, Application US/09905743B Patent No. 6828423 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) NAME/KEY: CDS

) LOCATION: (83)..(1669)

; OTHER INFORMATION:

US-09-905-743B-3
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEO ID NO 3
LENGTH: 2797
                                                                                                                           RESULT 14
US-09-905-743B-3
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                                                                                                                                                                 813 CATTCAGGTTGCAAGTAATGAAATTCTCAGGGACCCATGCTTTCATCCTGGATATAAGAA
                                                                                                                                         0; Gaps
                                                                                                           Query Match
Best Local Similarity 98.9%; Pred. No. 5.2e-78;
Matches 272; Conservative 0; Mismatches 3; Indels 0;
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; TYPE: DNA
; ORGANISM: Human
; ORGANISM:
; NAME/KEY: misc_feature
; LOCATION: (1)...(46885)
; GTHER INFORMATION: n = A,T,C or G
US-09-949-016-13848
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8; Search time 1041.08 Seconds (without alignments) 9228.876 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 25, Appl Sequence 1, Appli Sequence 1, Appli Sequence 29, Appl Sequence 1475, Ap Sequence 7, Appli Description US-10-646-308-29 US-10-641-643-1475 US-10-934-998-290 US-09-835-147-7 US-09-835-147-25 US-09-835-147-5 US-09-835-147-1 SUMMARIES 1437 1464 1365 1599 1599 1818 Length Query Match 97.4 97.4 95.0 91.8 91.8 1400 1319.2 1319.2 1319.2 1319.2 Score 1437 . Ю 10E4597 Result

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Sequence 25, Application US/09935147

Patent No. US2002000277A1

GENERAL INFORMATION:

APPLICANT: Maliszewski, Charles R.

APPLICANT: Gayle III, Richard B.

APPLICANT: Price, Virginia L.

APPLICANT: Gayle III, Richard B.

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment

FILE REFERENCE: 2879-US 5001-04-13

FILE REFERENCE: 2879-US 60/104,585

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1998-11-06

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 25

LEMPTH: 1464

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OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: construct of human CD39
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Best Local Similarity 98.2%; Pred. No. 0;
Matches 1437; Conservative 0; Mismatches
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NAME/KEY: CDS
LOCATION: (1).
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                                                               Query Match 100.0%; Score 1437; Best Local Similarity 100.0%; Pred. No. 0; Matches 1437; Conservative 0; Mismatches
   ; NAME/KEY: CDS
; LOCATION: (1)..(1434)
US-09-835-147-7
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                                                   TGTGCTCAGCCTTGGGAGGAGATAAAAACATCTTACGCTGGAGTAAAGGAGAAGTACCTG
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GENERAL INFORMATION

APPLICANT: Gayle III, Richard B.
APPLICANT: Gayle III, Richard B.
APPLICANT: Gimpel, Stewen D.
APPLICANT: Gimpel, Stewen D.
TITLE OF INVENTION: Inhibitors of Platelet Activation and Recrement Reference: 2879-08.
CURRENT APPLICATION NUMBER: US/09/835,147
CURRENT FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 60/104,585
PRIOR PLICATION NUMBER: US 60/104,666
PRIOR PLICATION NUMBER: US 60/107,466
PRIOR PLICATION NUMBER: US 60/109,010
PRIOR PLICATION NUMBER: US 60/149,010
PRIOR PLICATION NUMBER: PCT/US99/22955
PRIOR PLICATION NUMBER: PCT/US99/22955
PRIOR PLICATION NUMBER: PCT/US99/22955
PRIOR PLICATION NUMBER: DCT/US99/22955
PRIOR PLICATION NUMBER: DS-10-13
NUMBER OF SEQ ID NOS: 31
LENGTH: 1365
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95.0%; Score 1365; D)
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1365; Conservative 0; Mismatches
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US-09-835-147-5
Sequence 5, Application US/09835147
Patent No. US20020022277A1
GENERAL INFORMATION:
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Sequence 1, Application US/09835147

Sequence 1, Application US/09835147

Setent No. US20020002277A1

GENERAL INFORMATION:

APPLICANT: Maliszewski, Charles R.

APPLICANT: Gargel III, Richard B.

APPLICANT: Gimpel, Steven D.

TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment FILE REFERENCE: 2879-US

CURRENT APPLICATION NUMBER: US/09/835,147

CURRENT PELLON NUMBER: US 60/104.585

PRIOR FILING DATE: 1998-10-16

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PRIOR FILING DATE: 1998-11-06

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PRIOR FILING DATE: 1999-10-13

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Matches 1321; Conservative
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE FILE REFERENCE: 3432-B
CURRENT APPLICATION NUMBER: US/10/646,308
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: --to be assigned--
PRIOR APPLICATION NUMBER: 60/406,418
PRIOR FILING DATE: 2003-08-12
PRIOR PILING DATE: 2003-08-28
PRIOR FILING DATE: 2003-08-28
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 29
LENGTH: 1599
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                                                                                                                                                                                                                                                                                                                   Score 1319.2;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                     91.8%;
99.8%;
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.8
Matches 1321, Conservative
                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                   ) NAME/KEY: CDS
; LOCATION: (67)..(1596)
US-10-646-308-29
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99.8%; Pred. No. 0;
iive 0; Mismatches
              NAME: Zeller, Karen J.
REGIGTRATION NUMBER: 37,071
REFERENCÉ/DOCKET NUMBER: PA-0001 1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                   CLONE: 9765255
SEQUENCE DESCRIPTION: SEQ ID NO: 1475
                                                                                         INFORMATION FOR SEQ ID NO: 1475:
SEQUENCE CHARACTERISTICS:
                                                                                                                                          LENGTH: 1818 base pairs
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                    TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
                                                                                                                                                                                                                                                                                                                 Best Local Similarity >>..
Matches 1321; Conservative
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Best Local Similarity
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                                                  TTTACAAGACCCCCTGCACCAAGAGATTTGAGATGACTCTTCCATTCCAGCAGTTTGAAA
                                                                                                                TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACACCA
                                                                                                                                                            GTTACTGCCCTTACTCCCAGTGTGCCTTCAATGGGATTTTCTTGCCACCACTCCAGGGGG
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                                                                                              TCCAGGGTATTGGAAACTATCAACAATGCCATCAAAGCATCCTGGAGCTCTTCAACACCA
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Publication No. US20040077003A1
GENERAL INFORMATION:
Cocks, Benjamin G.
Suan G. Stuart
Jeffrey J. Selihamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
GENERAL OF STRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: INCYTE PHARMACEUTICALS,
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATE:
APPLICATION DATE:
FILING DATE: «Unknown»
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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US-10-641-643-1475
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                                                                                                          GGTTGACCCAGAACAAAGCATTGCCAGAAAACGTTAAGTATGGGATTGTGCTGGATGCGG
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i Sequence 290, Application US/10934998

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i Publication No. US20050153917A1

i Publication No. US20050153917A1

APPLICANT: AL-MAHMOOD, SALMAN

APPLICANT: COLIN, SYLVUE

i APPLICANT: AL-MAHMOOD, SALMAN

APPLICANT: AL-MAHMOOD, SALMAN

TITLE OF INVENTION: REPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF

TITLE OF INVENTION: REPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF

CURRENT APPLICATION NUMBER: US/10/934,998

CURRENT FILING DATE: 2004-09-03

PRIOR PPLING DATE: 2002-03-04

PRIOR PPLING DATE: 2002-03-04

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; DATABASE ENTRY DATE: 1995-04-12
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Publication No. US20050153917A1

GENERAL INFORMATION:

APPLICANT: AL-MAHMOOD, SALMAN

APPLICANT: CCLIN, SYLVIE

APPLICANT: CCLIN, SYLVIE

TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL

TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF

FILE REFERENCE: BMA-04-1206

CURRENT APPLICATION NUMBER: US/10/934,998

CURRENT APPLICATION NUMBER: PCT/FR03/00695

PRIOR PILING DATE: 2003-03-04

PRIOR FILING DATE: 2002-03-04

PRIOR FILING DATE: 2002-04-11

NUMBER OF SEQ ID NOS: 301

NUMBER OF SEQ ID NOS: 301

SSOFTWARE: PATCHTING VARIENCE: BATCHTING VARIENCE: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION NUMBER: PROSPERIOR APPLICATION
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91.8%; Score 1319.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches
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DATABASE ENTRY DATE: 2000-01-19

WELEVANT RESIDUES: (1)..(2081)

15-10-934-998-46
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OTHER INFORMATION: GS-N45
PUBLICATION INFORMATION:
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; GENERAL INFORMATION: APPLICANT: AL-WAHMOOD, SALWAN
; APPLICANT: AL-WAHMOOD, SALWAN
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GENEKAL INVOKATION:
GENEKAL INVOKATION:
APPLICANT: SHIFFMAN, DOV
APPLICANT: SHIFFMAN, DOV
APPLICANT: SOMGYTI, Roland
APPLICANT: SOMGYTI, Roland
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APPLICANT: SOMGYTI, Roland
APPLICANT: PORTER, Gordon J.
APPLICANT: PORTER, Gordon J.
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APPLICANT: PORTER, Gordon J.
APPLICANT: PORTER, SONGONOMBER: US/10/240,965
TITLE OF INVENTION NUMBER: US/10/240,965
CURRENT APPLICATION NUMBER: 00/195,106
FRIOR APPLICATION NUMBER: 60/195,106
FRIOR APPLICATION NUMBER: 60/195,106
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FRIOR APPLICATION NUMBER: 00/195,106
FRIOR APPLICATION NUMBER: 00/195,106
FRIOR APPLICATION INCOME
SOFTWARE: PEAL PROGRAM
SEQ ID NOS: 276
CURRENT: HOME GAPIENS
FRATURE: NAME/KEY: unisc feature
COTHER INFORMATION: Incyte ID NO. US20030165924AI 347965.2
FEATURE:
CONTRACTOR: 10 NOMER: 10 NO
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91.8%; Score 1319.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches
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OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                            Sequence 242, Application US/10240965
Publication No. US20030165924A1
GENERAL INFORMATION:
                                                          CCTA 1436
                                                                                                  CCTA 1634
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APPLICANT: SCHNEIDER, CHRISTOPHE
TITLE OF INVENTION: GENES INVOLVED IN REGULATING ANGIOGENESIS, PHARMACEUTICAL
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
FILE REFERENCE: BMA-04-1206
CURRENT APPLICATION NUMBER: US/10/934,998
CURRENT FILING DATE: 2004-09-03
PRIOR FILING DATE: 2003-03-04
PRIOR FILING DATE: 2003-03-04
PRIOR FILING DATE: 2002-04-11
PRIOR PLING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PATCHIN VERSION 3.2
SEQ ID NO 147
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US-10-934-998-193/c
; Sequence 193, Application US/10934998
; Publication No. US20050153917A1
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.5%;
Matches 642; Conservative 0
                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-934-998-147
                                                                                                                                                                           ID NO 147
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APPLICANT: AL-MAHMOOD, SALMAN
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APPLICANT: COLIN, SYLVIE
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APPLICANT: COLIN, SYLVIE
APPLICANT: COLING COLING CONTAINING SAME AND APPLICATIONS THEREOF
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
TITLE OF INVENTION: PREPARATIONS CONTAINING SAME AND APPLICATIONS THEREOF
CURRENT APPLICATION NUMBER: USCA-09-03
PRIOR PILING DATE: 2004-09-03
PRIOR PILING DATE: 2002-03-04
PRIOR PILING DATE: 2002-04-11
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PATENTING UND SECONO SID NOS: 301
SEQ ID NO 193
LENGTH: 6164
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CORGANISM: Homo sapiens
US-10-934-998-193
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Matches 642; Conserv
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Sequence 275, Application US/10002631C

Sequence 275, Application US/10002631C

Sequence 275, Application US/10002631C

Sequence 275, Application US/10002631C

SEDEMATION

APPLICANT: Muenster, Matthew

TITLE OF INVENTION: METHODS TO

SILE REPERENCE: A34943 090495.0243

CURRENT APPLICATION NUMBER: 00/10/002,631C

CURRENT FILING DATE: 2001-10-31

PRIOR APPLICATION NUMBER: 60/300,309

SIROR PILING DATE: 2001-06-21

NUMBER OF SEQ ID NOS: 324

SOFTWARE: FREISEQ for Windows Version 4.0
                                                                                                                                                                                                            Query Match
26.4%; Score 379; DB 10; L
Best Local Similarity 100.0%; Pred. No. 2.1e-109;
Matches 379; Conservative 0; Mismatches 0;
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                                                                                  | NAME/KEY: misc_feature
| LOCATION: (1)...(484)
| CTHER INFORMATION: n = A,T,C or G
US-09-918-995-23052
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; NAME/KEY: unsure
; LOCATION: (656)...(698)
; OTHER INFORMATION: n = A, C, US-10-002-631C-275
               TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 24656, Application US/09918995
| Publication No. US20030073623A1
| GENERAL INCORMATION:
| APPLICANT: Hyseq. Inc.
| TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: PROM VARIOUS cDNA LIBRARIES
| FILE REFERENCE: 20411-756
| CURRENT FILIG DATE: 2001-07-30
| PRIOR APPLICATION NUMBER: US/09/918,995
| PRIOR FILING DATE: 1999-01-20
| NUMBER OF SEQ ID NOS: 38054
| SOFTMARE: FRABESEQ for Windows Version 3.0
| SEQ ID NO 24656
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; Sequence 20052, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyeaq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/215,076
; PRIOR APPLICATION NUMBER: US/09/225,076
; PRIOR APPLICATION NUMBER: US/09/225,076
; NUMBER OF FOL INOS: 38054
; SOFTWARE: FERESEQ for Windows Version 3.0
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Best Local Similarity 96.69
Matches 423; Conservative
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US-09-918-995-24656
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US-09-918-995-23052
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Pred. No. 7e-81;
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APPLICANT: JIANG, FENG
TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF
FILE REFERENCE: UTSC: 658US
CURRENT APPLICATION NUMBER: US/09/923,304
CURRENT FILING DATE: 2001-08-06
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VET: 2.1
SOFTWARE: PATENTIN VET: 2.1
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Patent No. US20020081612A1
GENERAL INFORMATION:
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Best Local Similarity 54.3%;
Matches 707; Conservative (
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ORGANISM: Homo sapiens
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